

## WEST Search History

DATE: Wednesday, October 11, 2006

| Hide?                    | Set Name | Query   | Hit Count |
|--------------------------|----------|---|-----------|
|                          |          | <i>DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i> |           |
| <input type="checkbox"/> | L7       | L5 and L3   | 6         |
| <input type="checkbox"/> | L6       | L4 and L3   | 7         |
| <input type="checkbox"/> | L5       | Quanz-M\$.in.                                       | 29        |
| <input type="checkbox"/> | L4       | Buttcher-V\$.in.                                    | 14        |
| <input type="checkbox"/> | L3       | L1 and L2   | 35        |
| <input type="checkbox"/> | L2       | branching adj enzyme                                | 2611      |
| <input type="checkbox"/> | L1       | neisseria   | 8491      |

END OF SEARCH HISTORY

FILE 'AGRICOLA, BIOSIS, CAPLUS' ENTERED AT 15:22:51 ON 11 OCT 2006

|    |                         |
|----|-------------------------|
| L1 | 26961 S NEISSERIA       |
| L2 | 1784 S BRANCHING ENZYME |
| L3 | 5 S L1 AND L2           |
| L4 | 9 S BUTTCHER V?/AU      |
| L5 | 21 S QUANZ M?/AU        |
| L6 | 4 S L3 AND L5           |
| L7 | 3 S L3 AND L4           |

# SCORE Search Results Details for Application 10705195-1.rgc

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10705195 and Search Result us-10-705-1.rgc  
[start](#)

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 22, 2006, 19:21:51 ; Search time 13588 Seconds  
(without alignments)  
11647.768 Million cell updates/sec

Title: US-10-705-195-1  
Perfect score: 2475  
Sequence: 1 actgtatgccgtgcagctgg.....taaagcggcaccatactgcc 2475

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_env:\*  
2: gb\_pat:\*  
3: gb\_ph:\*  
4: gb\_pl:\*  
5: gb\_pr:\*  
6: gb\_ro:\*  
7: gb\_sts:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vi:\*  
11: gb\_ov:\*  
12: gb\_htg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID          | Description        |
|------------|-------|---------|--------------|----|-------------|--------------------|
| 1          | 2475  | 100.0   | 2475         | 2  | BD236814    | BD236814 Nucleic a |
| 2          | 2475  | 100.0   | 2475         | 2  | AR337816    | AR337816 Sequence  |
| 3          | 2475  | 100.0   | 2475         | 2  | AR479077    | AR479077 Sequence  |
| 4          | 2475  | 100.0   | 2475         | 2  | AX055494    | AX055494 Sequence  |
| 5          | 2475  | 100.0   | 2475         | 15 | AF102867    | AF102867 Neisseria |
| 6          | 941.6 | 38.0    | 2307         | 2  | AR387231    | AR387231 Sequence  |
| 7          | 894.6 | 36.1    | 2520         | 15 | AF434710    | AF434710 Pectobact |
| c 8        | 877.8 | 35.5    | 110000       | 15 | AE017220_36 | Continuation (37 o |
| c 9        | 876.2 | 35.4    | 110000       | 15 | CP000026_34 | Continuation (35 o |
| c 10       | 873   | 35.3    | 23506        | 15 | AE008863    | AE008863 Salmonell |
| 11         | 871.4 | 35.2    | 110000       | 15 | AE014613_41 | Continuation (42 o |
| 12         | 871.4 | 35.2    | 265050       | 15 | AL627281    | AL627281 Salmonell |
| c 13       | 858.8 | 34.7    | 110000       | 15 | AE014075_39 | Continuation (40 o |
| c 14       | 858.8 | 34.7    | 110000       | 15 | AE014075_40 | Continuation (41 o |
| c 15       | 849.2 | 34.3    | 110000       | 15 | CP000038_38 | Continuation (39 o |
| c 16       | 846   | 34.2    | 110000       | 15 | AE005174_43 | Continuation (44 o |
| c 17       | 846   | 34.2    | 110000       | 15 | U00096_35   | Continuation (36 o |
| 18         | 846   | 34.2    | 110000       | 15 | AP009048_40 | Continuation (41 o |
| c 19       | 846   | 34.2    | 110000       | 15 | BA000007_42 | Continuation (43 o |
| c 20       | 846   | 34.2    | 110000       | 15 | CP000036_34 | Continuation (35 o |
| c 21       | 845   | 34.1    | 72438        | 15 | ECOUW67_3   | Continuation (4 of |
| 22         | 844.4 | 34.1    | 2361         | 2  | BD071178    | BD071178 Plant lik |
| 23         | 844.4 | 34.1    | 2559         | 15 | ECOGLGBA    | M13751 Escherichia |
| c 24       | 841.2 | 34.0    | 110000       | 15 | AE005674_35 | Continuation (36 o |
| 25         | 841.2 | 34.0    | 110000       | 15 | AE014073_42 | Continuation (43 o |
| c 26       | 839.6 | 33.9    | 110000       | 15 | CP000034_33 | Continuation (34 o |
| c 27       | 837.4 | 33.8    | 110000       | 15 | BX950851_46 | Continuation (47 o |
| c 28       | 789.8 | 31.9    | 110000       | 15 | CP000057_16 | Continuation (17 o |
| c 29       | 789.8 | 31.9    | 349980       | 2  | CQ873160    | CQ873160 Sequence  |
| c 30       | 779.8 | 31.5    | 6306         | 2  | CQ872897    | CQ872897 Sequence  |
| 31         | 773.8 | 31.3    | 2055         | 2  | CS221362    | CS221362 Sequence  |
| 32         | 768   | 31.0    | 12144        | 15 | AE013993    | AE013993 Yersinia  |
| c 33       | 768   | 31.0    | 199050       | 15 | AJ414159    | AJ414159 Yersinia  |
| c 34       | 768   | 31.0    | 294253       | 15 | AE017139    | AE017139 Yersinia  |
| c 35       | 763.2 | 30.8    | 110000       | 15 | BX936398_44 | Continuation (45 o |
| 36         | 759.6 | 30.7    | 110000       | 2  | BD426631_14 | Continuation (15 o |
| 37         | 759.6 | 30.7    | 110000       | 2  | AR274513_14 | Continuation (15 o |
| 38         | 759.6 | 30.7    | 110000       | 2  | AR632719_14 | Continuation (15 o |
| 39         | 759.6 | 30.7    | 110000       | 15 | L42023_14   | Continuation (15 o |
| 40         | 758.2 | 30.6    | 12519        | 15 | AE006089    | AE006089 Pasteurel |
| c 41       | 752   | 30.4    | 110000       | 15 | AE016827_11 | Continuation (12 o |
| c 42       | 731.8 | 29.6    | 110000       | 15 | AP007255_33 | Continuation (34 o |
| c 43       | 704.6 | 28.5    | 110000       | 15 | CP000250_21 | Continuation (22 o |
| c 44       | 704.4 | 28.5    | 110000       | 15 | BX936398_45 | Continuation (46 o |
| 45         | 702.6 | 28.4    | 110000       | 15 | CP000230_29 | Continuation (30 o |

## ALIGNMENTS

## RESULT 1

BD236814

LOCUS BD236814 2475 bp DNA linear PAT 17-JUL-2003

DEFINITION Nucleic acid molecule encoding branching enzyme from Neisseria  
bacteria and process for producing alpha-1,6-branched  
alpha-1,4-glucane.

ACCESSION BD236814  
 VERSION BD236814.1 GI:33046584  
 KEYWORDS JP 2002527068-A/1.  
 SOURCE Bergeriella denitrificans  
 ORGANISM Bergeriella denitrificans  
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 Neisseriaceae; Bergeriella.  
 REFERENCE 1 (bases 1 to 2475)  
 AUTHORS Buttcher,V. and Quanz,M.  
 TITLE Nucleic acid molecule encoding branching enzyme from Neisseria  
 bacteria and process for producing alpha-1,6-branched  
 JOURNAL Patent: JP 2002527068-A 1 27-AUG-2002;  
 PLANTTEC BIOTECHNOLOGIE GMBH FORSCHUNG UND ENTWICKLUNG, MAX PLANCK  
 GESELLSCHAFT ZUR FOERDERUNG DER WISSENSCHAFTEN EV  
 COMMENT OS Neisseria denitrificans  
 PN JP 2002527068-A/1  
 PD 27-AUG-2002  
 PF 08-OCT-1999 JP 2000576030  
 PR 09-OCT-1998 DE 198 46 635.8,27-MAY-1999 DE 199 24 342.5 PI  
 VOLKER BUTTCHER,MARTIN QUANZ  
 PC C12N15/09,A01H5/00,C07K16/40,C12N1/15,C12N1/19,C12N1/21,C12N5/  
 PC 10,C12N9/10,  
 PC C12P19/04,C12N15/00,C12N5/00  
 CC Nucleic acid molecule encoding branching  
 enzyme from Neisseria  
 CC bacteria  
 CC and process for producing alpha-1,6-branched alpha-1,4-glucane  
 FH Key Location/Qualifiers  
 FT CDS (170)..(2458).  
 FEATURES Location/Qualifiers  
 source 1..2475  
 /organism="Bergeriella denitrificans"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:494"  
 ORIGIN

Query Match 100.0%; Score 2475; DB 2; Length 2475;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 1   | ACTGTATGCCGTGCAGCTGGAAAACCTGCTGGGCGTACGCGACAACCTCAATATTCCCGG | 60  |
|    |     |  |     |
| Db | 1   | ACTGTATGCCGTGCAGCTGGAAAACCTGCTGGGCGTACGCGACAACCTCAATATTCCCGG | 60  |
| Qy | 61  | CGTGGCCGAAGGCTATCCGAAGTGGGCGCGCAAATGCCGCAGCCTCTGGAAGCCTTTGC  | 120 |
|    |     |  |     |
| Db | 61  | CGTGGCCGAAGGCTATCCGAAGTGGGCGCGCAAATGCCGCAGCCTCTGGAAGCCTTTGC  | 120 |
| Qy | 121 | CCGCCACCCGCAAATGGGCAAGCAGCTTGCCATGATGGGAGACATCCGCATGAACCGAAA | 180 |
|    |     |  |     |
| Db | 121 | CCGCCACCCGCAAATGGGCAAGCAGCTTGCCATGATGGGAGACATCCGCATGAACCGAAA | 180 |
| Qy | 181 | CCGCCATATCCGACGCGGCTACCACCCGGAAGCCGAGAACGCCAAATCATCGACAGCCT  | 240 |
|    |     |  |     |
| Db | 181 | CCGCCATATCCGACGCGGCTACCACCCGGAAGCCGAGAACGCCAAATCATCGACAGCCT  | 240 |
| Qy | 241 | GTTTGCCGCCACCCACAGCGATCCGTTTGCCTATCTTGGGCGGCATCGTGTCAACGACGA | 300 |
|    |     |  |     |
| Db | 241 | GTTTGCCGCCACCCACAGCGATCCGTTTGCCTATCTTGGGCGGCATCGTGTCAACGACGA | 300 |
| Qy | 301 | ACGCGAAGCCGTGCGCGTGCTGCGTCCCGACGCGCACCACATCGACATCATCGACCGCCA | 360 |

|    |      |  |  |      |
|----|------|--|--|------|
| Db | 301  |  | ACGCGAAGCCGTGCGCGTGCTGCGTCCCGACGCGCACCACATCGACATCATCGACCGCCA | 360  |
| Qy | 361  |  | CACAGGCGCAGTCATCATGCCGTCTGAAAAATCGACGAGCGCGGCCTGTTTGCCGCCGT  | 420  |
| Db | 361  |  | CACAGGCGCAGTCATCATGCCGTCTGAAAAATCGACGAGCGCGGCCTGTTTGCCGCCGT  | 420  |
| Qy | 421  |  | ATTGCCCCAACACGCGCCCGACTACGCCCTGCTGGTGACATACCACGAGGGCGAAGCCGC | 480  |
| Db | 421  |  | ATTGCCCCAACACGCGCCCGACTACGCCCTGCTGGTGACATACCACGAGGGCGAAGCCGC | 480  |
| Qy | 481  |  | CGTACGCGAAGAAGATGACTACCGCTTCGGCAGCGCGCTGCAACATACCGATGCCTGGCT | 540  |
| Db | 481  |  | CGTACGCGAAGAAGATGACTACCGCTTCGGCAGCGCGCTGCAACATACCGATGCCTGGCT | 540  |
| Qy | 541  |  | GCTGGGCGAAGGCACGCACCTGCGCCCTTATGAAACGCTGGGCGCACATTTGCCGAAAT  | 600  |
| Db | 541  |  | GCTGGGCGAAGGCACGCACCTGCGCCCTTATGAAACGCTGGGCGCACATTTGCCGAAAT  | 600  |
| Qy | 601  |  | GGACGGCGTATCCGGCGTGCGCTTTGCCGTTTGGGCGCCCAACGCGCGGCGGGTATCGGT | 660  |
| Db | 601  |  | GGACGGCGTATCCGGCGTGCGCTTTGCCGTTTGGGCGCCCAACGCGCGGCGGGTATCGGT | 660  |
| Qy | 661  |  | CATCGGCGAATTCAACGGCTGGGACAGCCGCCCATGCCATGCGTCCGCACACAGGCAA   | 720  |
| Db | 661  |  | CATCGGCGAATTCAACGGCTGGGACAGCCGCCCATGCCATGCGTCCGCACACAGGCAA   | 720  |
| Qy | 721  |  | CGGCCTGTGGGACATCTTTATCCCCGGCGTCGGCCTCAACGCGCTGTATAAATTCTCCGT | 780  |
| Db | 721  |  | CGGCCTGTGGGACATCTTTATCCCCGGCGTCGGCCTCAACGCGCTGTATAAATTCTCCGT | 780  |
| Qy | 781  |  | ACTCGATGCCAACGGCAACATCCGCGAAAAAGCCGACCCCTACGCATTCGGCGCGGAGCT | 840  |
| Db | 781  |  | ACTCGATGCCAACGGCAACATCCGCGAAAAAGCCGACCCCTACGCATTCGGCGCGGAGCT | 840  |
| Qy | 841  |  | GCGCCCGACCAACGCATCCGTGGTGCGCGGCTTGCCGGCCAAAGCCGAAGCGCCGCTTT  | 900  |
| Db | 841  |  | GCGCCCGACCAACGCATCCGTGGTGCGCGGCTTGCCGGCCAAAGCCGAAGCGCCGCTTT  | 900  |
| Qy | 901  |  | CCGCCGCGCGCCAACCTCCGTGGAAGCGCCCATCAGCATTTACGAAGTCCATCTCGGCTC | 960  |
| Db | 901  |  | CCGCCGCGCGCCAACCTCCGTGGAAGCGCCCATCAGCATTTACGAAGTCCATCTCGGCTC | 960  |
| Qy | 961  |  | GTGGCGGCGCAATCCCGAAAACAATACTGGCTCACCTACACGCAGCTGGCCGACGAATT  | 1020 |
| Db | 961  |  | GTGGCGGCGCAATCCCGAAAACAATACTGGCTCACCTACACGCAGCTGGCCGACGAATT  | 1020 |
| Qy | 1021 |  | GGTGAACATATGTAAAAGACATGGGCTTCACCCACATCGAGCTGCTGCCCTTGTCGAATA | 1080 |
| Db | 1021 |  | GGTGAACATATGTAAAAGACATGGGCTTCACCCACATCGAGCTGCTGCCCTTGTCGAATA | 1080 |
| Qy | 1081 |  | TCCGTTTCGACGGCTCATGGGGCTACCAAGCCACCGGCCTGTATGCACCGACAGCCGCTT | 1140 |
| Db | 1081 |  | TCCGTTTCGACGGCTCATGGGGCTACCAAGCCACCGGCCTGTATGCACCGACAGCCGCTT | 1140 |
| Qy | 1141 |  | CGGCTCGCCCGATGAGCTGAAAGCCCTGATTGACGCCGCCACGCCCGGCATCAGCGT    | 1200 |
| Db | 1141 |  | CGGCTCGCCCGATGAGCTGAAAGCCCTGATTGACGCCGCCACGCCCGGCATCAGCGT    | 1200 |
| Qy | 1201 |  | GATTCTCGACTGGGTAGCGGGGCACTTCCCCACCGACGACCACGGCCTCAACACCTTCGA | 1260 |

## SCORE Search Results Details for Application 107 Search Result us-10-705-195-1.rng.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 10705195 and Search Result us-10-705-1.rng.  
[start](#)

[Go](#)

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 22, 2006, 19:15:26 ; Search time 1535 Seconds  
(without alignments)  
11241.899 Million cell updates/sec

Title: US-10-705-195-1  
Perfect score: 2475  
Sequence: 1 actgtatgccgtgcagctgg.....taaagcggcaccatactgcc 2475

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*  
15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result | No. | Score | Query Match | Length | DB | ID          | Description        |
|--------|-----|-------|-------------|--------|----|-------------|--------------------|
|        | 1   | 2475  | 100.0       | 2475   | 3  | AAA11731    | Aa11731 N. denitr  |
|        | 2   | 941.6 | 38.0        | 2307   | 11 | ACH98165    | Ach98165 Klebsiell |
|        | 3   | 846   | 34.2        | 2187   | 13 | ADT48837    | Adt48837 Bacterial |
|        | 4   | 844.4 | 34.1        | 2361   | 2  | AAV70952    | Aav70952 DNA seque |
| c      | 5   | 789.8 | 31.9        | 349980 | 13 | ADT05737    | Adt05737 Haemophil |
| c      | 6   | 779.8 | 31.5        | 6306   | 13 | ADT05474    | Adt05474 Haemophil |
|        | 7   | 759.6 | 30.7        | 110000 | 2  | AAT42063_14 | Continuation (15 o |
|        | 8   | 757.4 | 30.6        | 2193   | 8  | ACA34445    | Aca34445 Prokaryot |
|        | 9   | 690.2 | 27.9        | 2151   | 13 | ADS55782    | Ads55782 Bacterial |
|        | 10  | 680.6 | 27.5        | 2164   | 13 | ADT46098    | Adt46098 Bacterial |
|        | 11  | 678.6 | 27.4        | 2199   | 13 | ADS14563    | Ads14563 Pseudomon |
|        | 12  | 670.6 | 27.1        | 2472   | 11 | ABD09593    | Abd09593 Pseudomon |
|        | 13  | 663.6 | 26.8        | 2154   | 13 | ADS63589    | Ads63589 Bacterial |
|        | 14  | 663   | 26.8        | 2160   | 13 | ADS63965    | Ads63965 Bacterial |
|        | 15  | 663   | 26.8        | 2160   | 13 | ADT41565    | Adt41565 Bacterial |
|        | 16  | 657   | 26.5        | 2079   | 5  | AAS88840    | Aas88840 DNA encod |
|        | 17  | 647.8 | 26.2        | 2331   | 6  | ABQ90257    | Abq90257 M. capsul |
|        | 18  | 647.4 | 26.2        | 2214   | 13 | ADS60312    | Ads60312 Bacterial |
|        | 19  | 644.6 | 26.0        | 2163   | 13 | ADS62134    | Ads62134 Bacterial |
|        | 20  | 627.4 | 25.3        | 2142   | 13 | ADS63957    | Ads63957 Bacterial |
|        | 21  | 627.4 | 25.3        | 2142   | 13 | ADS64325    | Ads64325 Bacterial |
|        | 22  | 627.4 | 25.3        | 2142   | 13 | ADS63584    | Ads63584 Bacterial |
|        | 23  | 617.2 | 24.9        | 2172   | 14 | ACL68441    | Acl68441 M. xanthu |
|        | 24  | 617.2 | 24.9        | 2205   | 13 | ADT44556    | Adt44556 Bacterial |
| c      | 25  | 617.2 | 24.9        | 11276  | 14 | ACL64571    | Acl64571 M. xanthu |
|        | 26  | 593.6 | 24.0        | 2148   | 13 | ADT46962    | Adt46962 Bacterial |
|        | 27  | 567   | 22.9        | 2193   | 8  | ACF39411    | Acf39411 Mycobacte |
| c      | 28  | 567   | 22.9        | 110000 | 4  | AAI99682_14 | Continuation (15 o |
| c      | 29  | 554.4 | 22.4        | 110000 | 4  | AAI99683_14 | Continuation (15 o |
|        | 30  | 546.8 | 22.1        | 2118   | 13 | ADS45889    | Ads45889 Bacterial |
|        | 31  | 546   | 22.1        | 1884   | 13 | ADS57041    | Ads57041 Bacterial |
|        | 32  | 546   | 22.1        | 2034   | 10 | ADG18862    | Adg18862 DNA encod |
|        | 33  | 537.6 | 21.7        | 2178   | 13 | ADT44839    | Adt44839 Bacterial |
|        | 34  | 521.2 | 21.1        | 1434   | 5  | AAS93435    | Aas93435 DNA encod |
| c      | 35  | 521.2 | 21.1        | 1434   | 5  | AAS93857    | Aas93857 DNA encod |
|        | 36  | 512.2 | 20.7        | 2157   | 13 | ADS58032    | Ads58032 Bacterial |
|        | 37  | 510.2 | 20.6        | 349980 | 6  | ABQ81846    | Abq81846 Bifidobac |
|        | 38  | 510.2 | 20.6        | 349980 | 6  | ABQ81847    | Abq81847 Bifidobac |
|        | 39  | 504.8 | 20.4        | 22934  | 4  | AAS59613    | Aas59613 Propionib |
|        | 40  | 504.8 | 20.4        | 22934  | 8  | ACF64542    | Acf64542 Propionib |
| c      | 41  | 503.6 | 20.3        | 1701   | 11 | ABD09505    | Abd09505 Pseudomon |
|        | 42  | 471.4 | 19.0        | 2268   | 13 | ADT46200    | Adt46200 Bacterial |
|        | 43  | 457   | 18.5        | 1866   | 3  | AAC61606    | Aac61606 DNA encod |
|        | 44  | 457   | 18.5        | 1866   | 12 | ADH01235    | Adh01235 cDNA enco |
|        | 45  | 443.4 | 17.9        | 2313   | 13 | ADS48037    | Ads48037 Bacterial |

## ALIGNMENTS

## RESULT 1

AAA11731

ID AAA11731 standard; DNA; 2475 BP.

XX

AC AAA11731;

XX



DT 21-JUL-2000 (first entry)  
 XX  
 DE N. denitrificans alpha-1,6-branched alpha-1,4 glucan DNA.  
 XX  
 KW Alpha-1,6-branched alpha-1,4-glucan; branching enzyme; binder; carrier;  
 KW transgenic plant; flavor; perfume; packaging material; papermaking;  
 KW ultra-violet light adsorber; starch; textile; wetting agent; ds.  
 XX  
 OS Neisseria denitrificans.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 170. .2458  
 FT /\*tag= a  
 FT /product= "alpha-1,6-branched alpha-1,4-glucan"  
 XX  
 PN WO200022140-A1.  
 XX  
 PD 20-APR-2000.  
 XX  
 PF 08-OCT-1999; 99WO-EP007562.  
 XX  
 PR 09-OCT-1998; 98DE-01046635.  
 PR 27-MAY-1999; 99DE-01024342.  
 XX  
 PA (PLAN-) PLANTTEC BIOTECHNOLOGIE GMBH.  
 PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX  
 PI Buettcher V, Quanz M;  
 XX  
 DR WPI; 2000-317992/27.  
 DR P-PSDB; AAW90977.  
 XX  
 PT New nucleic acid encoding a branching enzyme, useful for in vitro  
 PT synthesis of branched glucans and to prepare transgenic plants producing  
 PT modified starch.  
 XX  
 PS Claim 1b; Page 93-96; 115pp; German.  
 XX  
 CC This invention describes a novel nucleic acid (I) isolated from Neisseria  
 CC which encodes a branching enzyme (II). (I) is used for recombinant  
 CC production of (II) subsequently used in the in vitro production of alpha-  
 CC 1,6-branched alpha-1,4-glucans. It is also used to prepare transgenic  
 CC plants that produce starches with modified properties. (III) are used as  
 CC binders for tablets, carriers for pharmaceuticals, flavors and perfumes  
 CC and powdered additives, packaging materials, ultra-violet light adsorbers  
 CC in sunscreens and also for any of the usual applications of starch in  
 CC foods, papermaking, as textile size, in soil stabilization, as wetting  
 CC agent for agricultural chemicals, as polymer additives etc. Fragments of  
 CC (I) are useful as PCR primers and antisense molecules or ribozymes for  
 CC inhibiting expression of (I), and the regulatory region of (II) can be  
 CC used to control expression of heterologous sequences in host cells. (I)  
 CC provides an inexpensive method for producing alpha-1,6-branched alpha-1,4  
 CC -glucans (III), producing products that can be tailored for particular  
 CC applications, particularly by controlling the degree of branching. Starch  
 CC from transgenic plants has increased gel strength; reduced phosphate  
 CC content; reduced peak viscosity; lower pasting temperature and granule  
 CC size and/or altered sidechain distribution. This sequence encodes an  
 CC alpha-1,6-branched alpha-1,4-glucan isolated from Neisseria denitrificans  
 CC which is described in the method of the invention  
 XX  
 SQ Sequence 2475 BP; 560 A; 827 C; 674 G; 414 T; 0 U; 0 Other;

Query Match 100.0%; Score 2475; DB 3; Length 2475;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 1   | ACTGTATGCCGTGCAGCTGGAAAACCTGCTGGGCGTACGCGACAACCTCAATATTCCCGG | 60  |
|    |     |  |     |
| Db | 1   | ACTGTATGCCGTGCAGCTGGAAAACCTGCTGGGCGTACGCGACAACCTCAATATTCCCGG | 60  |
| Qy | 61  | CGTGGCCGAAGGCTATCCGAACCTGGGCGCGCAAAATGCCGAGCCTCTGGAAGCCTTTGC | 120 |
|    |     |  |     |
| Db | 61  | CGTGGCCGAAGGCTATCCGAACCTGGGCGCGCAAAATGCCGAGCCTCTGGAAGCCTTTGC | 120 |
| Qy | 121 | CCGCCACCCGCAAATGGGCAAGCAGCTTGCCATGATGGGAGACATCCGCATGAACCGAAA | 180 |
|    |     |  |     |
| Db | 121 | CCGCCACCCGCAAATGGGCAAGCAGCTTGCCATGATGGGAGACATCCGCATGAACCGAAA | 180 |
| Qy | 181 | CCGCCATATCCGACGCGGTACCACCCGGAAGCCGAGAACGCCAAATCATCGACAGCCT   | 240 |
|    |     |  |     |
| Db | 181 | CCGCCATATCCGACGCGGTACCACCCGGAAGCCGAGAACGCCAAATCATCGACAGCCT   | 240 |
| Qy | 241 | GTTTGCCGCCACCCACAGCGATCCGTTTGCCTATCTTGGGCGGCATCGTGTCAACGACGA | 300 |
|    |     |  |     |
| Db | 241 | GTTTGCCGCCACCCACAGCGATCCGTTTGCCTATCTTGGGCGGCATCGTGTCAACGACGA | 300 |
| Qy | 301 | ACGCGAAGCCGTGCGCGTGCTGCGTCCCGACGCGCACCATCGACATCATCGACCGCCA   | 360 |
|    |     |  |     |
| Db | 301 | ACGCGAAGCCGTGCGCGTGCTGCGTCCCGACGCGCACCATCGACATCATCGACCGCCA   | 360 |
| Qy | 361 | CACAGGCGCAGTCATCATGCCGTCTGAAAAAATCGACGAGCGCGGCCTGTTTGCCGCCGT | 420 |
|    |     |  |     |
| Db | 361 | CACAGGCGCAGTCATCATGCCGTCTGAAAAAATCGACGAGCGCGGCCTGTTTGCCGCCGT | 420 |
| Qy | 421 | ATTGCCCGAACACGCGCCCGACTACGCCCTGCTGGTGACATACCACGAGGGCGAAGCCGC | 480 |
|    |     |  |     |
| Db | 421 | ATTGCCCGAACACGCGCCCGACTACGCCCTGCTGGTGACATACCACGAGGGCGAAGCCGC | 480 |
| Qy | 481 | CGTACGCGAAGAAGATGACTACCGCTTCGGCAGCGCGCTGCAACATACCGATGCCTGGCT | 540 |
|    |     |  |     |
| Db | 481 | CGTACGCGAAGAAGATGACTACCGCTTCGGCAGCGCGCTGCAACATACCGATGCCTGGCT | 540 |
| Qy | 541 | GCTGGGCGAAGGCACGCACCTGCGCCCTTATGAAACGCTGGGCGCACATTTGCCGAAAT  | 600 |
|    |     |  |     |
| Db | 541 | GCTGGGCGAAGGCACGCACCTGCGCCCTTATGAAACGCTGGGCGCACATTTGCCGAAAT  | 600 |
| Qy | 601 | GGACGGCGTATCCGGCGTGCGCTTTGCCGTTTGGGCGCCCAACGCGCGGGGTATCGGT   | 660 |
|    |     |  |     |
| Db | 601 | GGACGGCGTATCCGGCGTGCGCTTTGCCGTTTGGGCGCCCAACGCGCGGGGTATCGGT   | 660 |
| Qy | 661 | CATCGGCGAATTCAACGGCTGGGACAGCCGCCCATGCCATGCGTCCGCACACAGGCAA   | 720 |
|    |     |  |     |
| Db | 661 | CATCGGCGAATTCAACGGCTGGGACAGCCGCCCATGCCATGCGTCCGCACACAGGCAA   | 720 |
| Qy | 721 | CGGCCTGTGGGACATCTTTATCCCCGGCGTCGGCCTCAACGCGCTGTATAAATTCTCCGT | 780 |
|    |     |  |     |
| Db | 721 | CGGCCTGTGGGACATCTTTATCCCCGGCGTCGGCCTCAACGCGCTGTATAAATTCTCCGT | 780 |
| Qy | 781 | ACTCGATGCCAACGGCAACATCCGCGAAAAAGCCGACCCCTACGCATTGCGCGCGGAGCT | 840 |
|    |     |  |     |
| Db | 781 | ACTCGATGCCAACGGCAACATCCGCGAAAAAGCCGACCCCTACGCATTGCGCGCGGAGCT | 840 |

# SCORE Search Results Details for Application 10705195 and Search Result us-10-705-195-1.rni.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments](#) / [Suggest](#)

This page gives you Search Results detail for the Application 10705195 and Search Result us-10-705-195-1.rni.  
[start](#)

[Go Back to](#)

GenCore version 5.1.9  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 22, 2006, 19:27:21 ; Search time 466 Seconds  
 (without alignments)  
 9937.756 Million cell updates/sec

Title: US-10-705-195-1  
 Perfect score: 2475  
 Sequence: 1 actgtatgccgtgcagctgg.....taaagcggcaccatactgcc 2475

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*  
 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*  
 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*  
 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*  
 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| -----      |       |             |        |    |             |

|      |       |       |         |   |                     |                   |
|------|-------|-------|---------|---|---------------------|-------------------|
| 1    | 2475  | 100.0 | 2475    | 3 | US-09-579-365-1     | Sequence 1, Appli |
| 2    | 2475  | 100.0 | 2475    | 3 | US-09-807-063-1     | Sequence 1, Appli |
| 3    | 941.6 | 38.0  | 2307    | 3 | US-09-489-039A-3960 | Sequence 3960, Ap |
| 4    | 759.6 | 30.7  | 1830121 | 3 | US-09-557-884-1     | Sequence 1, Appli |
| 5    | 759.6 | 30.7  | 1830121 | 3 | US-09-643-990A-1    | Sequence 1, Appli |
| 6    | 759.6 | 30.7  | 1830121 | 3 | US-10-158-865-1     | Sequence 1, Appli |
| 7    | 670.6 | 27.1  | 2472    | 3 | US-09-252-991A-8197 | Sequence 8197, Ap |
| 8    | 617.2 | 24.9  | 2172    | 3 | US-09-902-540-4904  | Sequence 4904, Ap |
| c 9  | 617.2 | 24.9  | 11276   | 3 | US-09-902-540-1034  | Sequence 1034, Ap |
| c 10 | 567   | 22.9  | 4411529 | 3 | US-09-103-840A-1    | Sequence 1, Appli |
| c 11 | 554.4 | 22.4  | 4403765 | 3 | US-09-103-840A-2    | Sequence 2, Appli |
| c 12 | 503.6 | 20.3  | 1701    | 3 | US-09-252-991A-8109 | Sequence 8109, Ap |
| 13   | 457   | 18.5  | 1866    | 3 | US-09-537-120-1     | Sequence 1, Appli |
| 14   | 370   | 14.9  | 1308    | 3 | US-09-252-991A-8131 | Sequence 8131, Ap |
| 15   | 324.2 | 13.1  | 2426    | 3 | US-08-528-026C-3    | Sequence 3, Appli |
| 16   | 314.6 | 12.7  | 36470   | 3 | US-08-311-731A-123  | Sequence 123, App |
| c 17 | 314.6 | 12.7  | 1230025 | 3 | US-09-198-452A-1    | Sequence 1, Appli |
| c 18 | 314.6 | 12.7  | 1230230 | 3 | US-09-438-185A-1    | Sequence 1, Appli |
| 19   | 277.6 | 11.2  | 1877    | 5 | US-09-974-300-653   | Sequence 653, App |
| 20   | 201.8 | 8.2   | 1929    | 3 | US-09-583-110-1148  | Sequence 1148, Ap |
| 21   | 201.8 | 8.2   | 1956    | 3 | US-09-107-433-242   | Sequence 242, App |
| c 22 | 186.6 | 7.5   | 11384   | 3 | US-08-961-527-45    | Sequence 45, Appl |
| c 23 | 167   | 6.7   | 702     | 3 | US-09-252-991A-8108 | Sequence 8108, Ap |
| 24   | 161.4 | 6.5   | 807     | 3 | US-09-634-238-168   | Sequence 168, App |
| 25   | 157   | 6.3   | 976     | 3 | US-08-961-083-79    | Sequence 79, Appl |
| 26   | 157   | 6.3   | 976     | 3 | US-09-536-784-79    | Sequence 79, Appl |
| 27   | 157   | 6.3   | 976     | 3 | US-09-765-271-79    | Sequence 79, Appl |
| 28   | 157   | 6.3   | 976     | 3 | US-09-765-272A-79   | Sequence 79, Appl |
| c 29 | 119.2 | 4.8   | 781     | 3 | US-09-902-540-1586  | Sequence 1586, Ap |
| 30   | 119   | 4.8   | 780     | 3 | US-09-902-540-2210  | Sequence 2210, Ap |
| 31   | 101.2 | 4.1   | 290     | 3 | US-08-651-155B-188  | Sequence 188, App |
| 32   | 101.2 | 4.1   | 290     | 3 | US-09-194-036B-188  | Sequence 188, App |
| 33   | 100.6 | 4.1   | 5402    | 3 | US-09-221-017B-194  | Sequence 194, App |
| 34   | 93.4  | 3.8   | 461     | 3 | US-09-634-238-167   | Sequence 167, App |
| 35   | 93    | 3.8   | 356     | 3 | US-09-634-238-169   | Sequence 169, App |
| c 36 | 87.6  | 3.5   | 4125    | 3 | US-09-252-991A-8065 | Sequence 8065, Ap |
| 37   | 80.4  | 3.2   | 1896    | 3 | US-09-902-540-6849  | Sequence 6849, Ap |
| c 38 | 80.4  | 3.2   | 5043    | 3 | US-09-902-540-574   | Sequence 574, App |
| c 39 | 78.8  | 3.2   | 1770    | 3 | US-09-252-991A-8263 | Sequence 8263, Ap |
| 40   | 78.8  | 3.2   | 1947    | 3 | US-09-252-991A-8057 | Sequence 8057, Ap |
| 41   | 73.8  | 3.0   | 2955    | 4 | US-09-880-107-2148  | Sequence 2148, Ap |
| 42   | 69.4  | 2.8   | 2307    | 3 | US-09-786-480B-1    | Sequence 1, Appli |
| 43   | 67.8  | 2.7   | 2554    | 5 | US-10-162-948-1     | Sequence 1, Appli |
| 44   | 67.8  | 2.7   | 2853    | 3 | US-09-609-040-3     | Sequence 3, Appli |
| 45   | 67.2  | 2.7   | 2223    | 3 | US-09-297-703C-43   | Sequence 43, Appl |

## ALIGNMENTS

## RESULT 1

US-09-579-365-1

; Sequence 1, Application US/09579365

; Patent No. 6566585

; GENERAL INFORMATION:

; APPLICANT: Martin QUANZ

; TITLE OF INVENTION: GENETICALLY MODIFIED PLANT CELLS AND PLANTS WITH AN

; TITLE OF INVENTION: INCREASED ACTIVITY OF AN AMYLOSUCRASE PROTEIN AND A

; TITLE OF INVENTION: BRANCHING ENZYME

; FILE REFERENCE: 0147-0200P

; CURRENT APPLICATION NUMBER: US/09/579,365

; CURRENT FILING DATE: 2000-05-25  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 2475  
 ; TYPE: DNA  
 ; ORGANISM: Neisseria denitrificans  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (170)..(2458)  
 US-09-579-365-1

Query Match 100.0%; Score 2475; DB 3; Length 2475;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 1   | ACTGTATGCCGTGCAGCTGGAAAACCTGCTGGGCGTACGCGACAACCTCAATATTCCCGG | 60  |
|    |     |  |     |
| Db | 1   | ACTGTATGCCGTGCAGCTGGAAAACCTGCTGGGCGTACGCGACAACCTCAATATTCCCGG | 60  |
| Qy | 61  | CGTGGCCGAAGGCTATCCGAAGTGGGCGCGCAAATGCCGAGCCTCTGGAAGCCTTTGC   | 120 |
|    |     |  |     |
| Db | 61  | CGTGGCCGAAGGCTATCCGAAGTGGGCGCGCAAATGCCGAGCCTCTGGAAGCCTTTGC   | 120 |
| Qy | 121 | CCGCCACCCGCAAATGGGCAAGCAGCTTGCCATGATGGGAGACATCCGCATGAACCGAAA | 180 |
|    |     |  |     |
| Db | 121 | CCGCCACCCGCAAATGGGCAAGCAGCTTGCCATGATGGGAGACATCCGCATGAACCGAAA | 180 |
| Qy | 181 | CCGCCATATCCGACGCGGCTACCACCCGGAAGCCGAGAACGCCAAATCATCGACAGCCT  | 240 |
|    |     |  |     |
| Db | 181 | CCGCCATATCCGACGCGGCTACCACCCGGAAGCCGAGAACGCCAAATCATCGACAGCCT  | 240 |
| Qy | 241 | GTTTGCCGCCACCCACAGCGATCCGTTTGCCTATCTTGGGCGGCATCGTGTCAACGACGA | 300 |
|    |     |  |     |
| Db | 241 | GTTTGCCGCCACCCACAGCGATCCGTTTGCCTATCTTGGGCGGCATCGTGTCAACGACGA | 300 |
| Qy | 301 | ACGCGAAGCCGTGCGCGTGCTGCGTCCCGACGCGCACCACATCGACATCATCGACCGCCA | 360 |
|    |     |  |     |
| Db | 301 | ACGCGAAGCCGTGCGCGTGCTGCGTCCCGACGCGCACCACATCGACATCATCGACCGCCA | 360 |
| Qy | 361 | CACAGGCGCAGTCATCATGCCGTCTGAAAAATCGACGAGCGCGGCCTGTTTGCCGCCGT  | 420 |
|    |     |  |     |
| Db | 361 | CACAGGCGCAGTCATCATGCCGTCTGAAAAATCGACGAGCGCGGCCTGTTTGCCGCCGT  | 420 |
| Qy | 421 | ATTGCCCGAACACGCGCCCGACTACGCCCTGCTGGTGACATACCACGAGGGCGAAGCCGC | 480 |
|    |     |  |     |
| Db | 421 | ATTGCCCGAACACGCGCCCGACTACGCCCTGCTGGTGACATACCACGAGGGCGAAGCCGC | 480 |
| Qy | 481 | CGTACGCGAAGAAGATGACTACCGCTTCGGCAGCGCGCTGCAACATACCGATGCCTGGCT | 540 |
|    |     |  |     |
| Db | 481 | CGTACGCGAAGAAGATGACTACCGCTTCGGCAGCGCGCTGCAACATACCGATGCCTGGCT | 540 |
| Qy | 541 | GCTGGGCGAAGGCACGCACCTGCGCCCTTATGAAACGCTGGGCGCACATTTGCGCGAAAT | 600 |
|    |     |  |     |
| Db | 541 | GCTGGGCGAAGGCACGCACCTGCGCCCTTATGAAACGCTGGGCGCACATTTGCGCGAAAT | 600 |
| Qy | 601 | GGACGGCGTATCCGGCGTGCGCTTTGCCGTTTGGGCGCCCAACGCGCGGCGGGTATCGGT | 660 |
|    |     |  |     |
| Db | 601 | GGACGGCGTATCCGGCGTGCGCTTTGCCGTTTGGGCGCCCAACGCGCGGCGGGTATCGGT | 660 |
| Qy | 661 | CATCGGCGAATTCAACGGCTGGGACAGCCGCCCATGCCATGCGTCCGCACACAGGCAA   | 720 |

|    |      |  |      |
|----|------|--|------|
| Db | 661  | <br>CATCGGCGAATTCAACGGCTGGGACAGCCGCCCATGCCATGCGTCCGCACACAGGCAA     | 720  |
| Qy | 721  | CGGCCTGTGGGACATCTTTATCCCCGGCGTCGGCCTCAACGCGCTGTATAAATTCTCCGT       | 780  |
| Db | 721  | <br>CGGCCTGTGGGACATCTTTATCCCCGGCGTCGGCCTCAACGCGCTGTATAAATTCTCCGT   | 780  |
| Qy | 781  | ACTCGATGCCAACGGCAACATCCGCGAAAAAGCCGACCCCTACGCATTGCGCGCGGAGCT       | 840  |
| Db | 781  | <br>ACTCGATGCCAACGGCAACATCCGCGAAAAAGCCGACCCCTACGCATTGCGCGCGGAGCT   | 840  |
| Qy | 841  | GCGCCCGACCAACGCATCCGTGGTGC GCGGCTTGCCGGCCAAAGCCGAAGCGCCGCTTT       | 900  |
| Db | 841  | <br>GCGCCCGACCAACGCATCCGTGGTGC GCGGCTTGCCGGCCAAAGCCGAAGCGCCGCTTT   | 900  |
| Qy | 901  | CCGCCGCGCGCCAACTCCGTGGAAGCGCCCATCAGCATTTACGAAGTCCATCTCGGCTC        | 960  |
| Db | 901  | <br>CCGCCGCGCGCCAACTCCGTGGAAGCGCCCATCAGCATTTACGAAGTCCATCTCGGCTC    | 960  |
| Qy | 961  | GTGGCGGCGCAATCCCGAAAACAATACTGGCTCACCTACACGCAGCTGGCCGACGAATT        | 1020 |
| Db | 961  | <br>GTGGCGGCGCAATCCCGAAAACAATACTGGCTCACCTACACGCAGCTGGCCGACGAATT    | 1020 |
| Qy | 1021 | GGTGAAGTATGTAAAAGACATGGGCTTCACCCACATCGAGCTGCTGCCCTTGTCGAATA        | 1080 |
| Db | 1021 | <br>GGTGAAGTATGTAAAAGACATGGGCTTCACCCACATCGAGCTGCTGCCCTTGTCGAATA    | 1080 |
| Qy | 1081 | TCCGTTTCGACGGCTCATGGGGCTACCAAGCCACCGGCCTGTATGCACCGACGAGCCGCTT      | 1140 |
| Db | 1081 | <br>TCCGTTTCGACGGCTCATGGGGCTACCAAGCCACCGGCCTGTATGCACCGACGAGCCGCTT  | 1140 |
| Qy | 1141 | CGGCTCGCCCGATGAGCTGAAAGCCCTGATTGACGCCGCCACGCCGCGGCATCAGCGT         | 1200 |
| Db | 1141 | <br>CGGCTCGCCCGATGAGCTGAAAGCCCTGATTGACGCCGCCACGCCGCGGCATCAGCGT     | 1200 |
| Qy | 1201 | GATTCTCGACTGGGTAGCGGGGCACTTCCCCACCGACGACCAACGGCCTCAACACCTTCGA      | 1260 |
| Db | 1201 | <br>GATTCTCGACTGGGTAGCGGGGCACTTCCCCACCGACGACCAACGGCCTCAACACCTTCGA  | 1260 |
| Qy | 1261 | CGGCACGGCGCTTTACGAACACGCCGACCCGCGCGAAGGCTACCATCAGGATTGGAACAC       | 1320 |
| Db | 1261 | <br>CGGCACGGCGCTTTACGAACACGCCGACCCGCGCGAAGGCTACCATCAGGATTGGAACAC   | 1320 |
| Qy | 1321 | GCTGATTTACAACCTTCGGCCGCAACGAAGTCAAAAACCTTCCTGCAGGGCAACGCGCTCTA     | 1380 |
| Db | 1321 | <br>GCTGATTTACAACCTTCGGCCGCAACGAAGTCAAAAACCTTCCTGCAGGGCAACGCGCTCTA | 1380 |
| Qy | 1381 | CTGGATTGAGCGTTTCGGCTTCGACGGCATCCGCGTGGACGCCGTGGCCTCGATGATTTA       | 1440 |
| Db | 1381 | <br>CTGGATTGAGCGTTTCGGCTTCGACGGCATCCGCGTGGACGCCGTGGCCTCGATGATTTA   | 1440 |
| Qy | 1441 | CCGCAACTACTCGCGCAAAGACGGCGAGTGGATTCCCAACCGCTACGGCGGCAGCGAAAA       | 1500 |
| Db | 1441 | <br>CCGCAACTACTCGCGCAAAGACGGCGAGTGGATTCCCAACCGCTACGGCGGCAGCGAAAA   | 1500 |
| Qy | 1501 | TCTGGAAGCCATCGCCTTTTTGCGCCAAACCAATGCCGTCTTAAAAAGCGAAACACCCGG       | 1560 |
| Db | 1501 | <br>TCTGGAAGCCATCGCCTTTTTGCGCCAAACCAATGCCGTCTTAAAAAGCGAAACACCCGG   | 1560 |
| Qy | 1561 | CGCCGGCTCGTTTGCCGAAGAATCGACTTCCTTTGCCGACGTAACCCGCGAAGCCGGCCT       | 1620 |
|    |      |  |      |

# SCORE Search Results Details for Application 10705195 and Search Result us-10-705-195-1.rni.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments](#) / [Suggest](#)

This page gives you Search Results detail for the Application 10705195 and Search Result us-10-705-195-1.rni.  
[start](#)

[Go Back to](#)

GenCore version 5.1.9  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 22, 2006, 19:27:21 ; Search time 466 Seconds  
 (without alignments)  
 9937.756 Million cell updates/sec

Title: US-10-705-195-1  
 Perfect score: 2475  
 Sequence: 1 actgtatgccgtgcagctgg.....taaagcggcaccatactgcc 2475

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*  
 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*  
 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*  
 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*  
 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| -----      |       |             |        |       |             |

|   |    |       |       |         |   |                     |                   |
|---|----|-------|-------|---------|---|---------------------|-------------------|
|   | 1  | 2475  | 100.0 | 2475    | 3 | US-09-579-365-1     | Sequence 1, Appli |
|   | 2  | 2475  | 100.0 | 2475    | 3 | US-09-807-063-1     | Sequence 1, Appli |
|   | 3  | 941.6 | 38.0  | 2307    | 3 | US-09-489-039A-3960 | Sequence 3960, Ap |
|   | 4  | 759.6 | 30.7  | 1830121 | 3 | US-09-557-884-1     | Sequence 1, Appli |
|   | 5  | 759.6 | 30.7  | 1830121 | 3 | US-09-643-990A-1    | Sequence 1, Appli |
|   | 6  | 759.6 | 30.7  | 1830121 | 3 | US-10-158-865-1     | Sequence 1, Appli |
|   | 7  | 670.6 | 27.1  | 2472    | 3 | US-09-252-991A-8197 | Sequence 8197, Ap |
|   | 8  | 617.2 | 24.9  | 2172    | 3 | US-09-902-540-4904  | Sequence 4904, Ap |
| c | 9  | 617.2 | 24.9  | 11276   | 3 | US-09-902-540-1034  | Sequence 1034, Ap |
| c | 10 | 567   | 22.9  | 4411529 | 3 | US-09-103-840A-1    | Sequence 1, Appli |
| c | 11 | 554.4 | 22.4  | 4403765 | 3 | US-09-103-840A-2    | Sequence 2, Appli |
| c | 12 | 503.6 | 20.3  | 1701    | 3 | US-09-252-991A-8109 | Sequence 8109, Ap |
|   | 13 | 457   | 18.5  | 1866    | 3 | US-09-537-120-1     | Sequence 1, Appli |
|   | 14 | 370   | 14.9  | 1308    | 3 | US-09-252-991A-8131 | Sequence 8131, Ap |
|   | 15 | 324.2 | 13.1  | 2426    | 3 | US-08-528-026C-3    | Sequence 3, Appli |
|   | 16 | 314.6 | 12.7  | 36470   | 3 | US-08-311-731A-123  | Sequence 123, App |
| c | 17 | 314.6 | 12.7  | 1230025 | 3 | US-09-198-452A-1    | Sequence 1, Appli |
| c | 18 | 314.6 | 12.7  | 1230230 | 3 | US-09-438-185A-1    | Sequence 1, Appli |
|   | 19 | 277.6 | 11.2  | 1877    | 5 | US-09-974-300-653   | Sequence 653, App |
|   | 20 | 201.8 | 8.2   | 1929    | 3 | US-09-583-110-1148  | Sequence 1148, Ap |
|   | 21 | 201.8 | 8.2   | 1956    | 3 | US-09-107-433-242   | Sequence 242, App |
| c | 22 | 186.6 | 7.5   | 11384   | 3 | US-08-961-527-45    | Sequence 45, Appl |
| c | 23 | 167   | 6.7   | 702     | 3 | US-09-252-991A-8108 | Sequence 8108, Ap |
|   | 24 | 161.4 | 6.5   | 807     | 3 | US-09-634-238-168   | Sequence 168, App |
|   | 25 | 157   | 6.3   | 976     | 3 | US-08-961-083-79    | Sequence 79, Appl |
|   | 26 | 157   | 6.3   | 976     | 3 | US-09-536-784-79    | Sequence 79, Appl |
|   | 27 | 157   | 6.3   | 976     | 3 | US-09-765-271-79    | Sequence 79, Appl |
|   | 28 | 157   | 6.3   | 976     | 3 | US-09-765-272A-79   | Sequence 79, Appl |
| c | 29 | 119.2 | 4.8   | 781     | 3 | US-09-902-540-1586  | Sequence 1586, Ap |
|   | 30 | 119   | 4.8   | 780     | 3 | US-09-902-540-2210  | Sequence 2210, Ap |
|   | 31 | 101.2 | 4.1   | 290     | 3 | US-08-651-155B-188  | Sequence 188, App |
|   | 32 | 101.2 | 4.1   | 290     | 3 | US-09-194-036B-188  | Sequence 188, App |
|   | 33 | 100.6 | 4.1   | 5402    | 3 | US-09-221-017B-194  | Sequence 194, App |
|   | 34 | 93.4  | 3.8   | 461     | 3 | US-09-634-238-167   | Sequence 167, App |
|   | 35 | 93    | 3.8   | 356     | 3 | US-09-634-238-169   | Sequence 169, App |
| c | 36 | 87.6  | 3.5   | 4125    | 3 | US-09-252-991A-8065 | Sequence 8065, Ap |
|   | 37 | 80.4  | 3.2   | 1896    | 3 | US-09-902-540-6849  | Sequence 6849, Ap |
| c | 38 | 80.4  | 3.2   | 5043    | 3 | US-09-902-540-574   | Sequence 574, App |
| c | 39 | 78.8  | 3.2   | 1770    | 3 | US-09-252-991A-8263 | Sequence 8263, Ap |
|   | 40 | 78.8  | 3.2   | 1947    | 3 | US-09-252-991A-8057 | Sequence 8057, Ap |
|   | 41 | 73.8  | 3.0   | 2955    | 4 | US-09-880-107-2148  | Sequence 2148, Ap |
|   | 42 | 69.4  | 2.8   | 2307    | 3 | US-09-786-480B-1    | Sequence 1, Appli |
|   | 43 | 67.8  | 2.7   | 2554    | 5 | US-10-162-948-1     | Sequence 1, Appli |
|   | 44 | 67.8  | 2.7   | 2853    | 3 | US-09-609-040-3     | Sequence 3, Appli |
|   | 45 | 67.2  | 2.7   | 2223    | 3 | US-09-297-703C-43   | Sequence 43, Appl |

## ALIGNMENTS

## RESULT 1

US-09-579-365-1

; Sequence 1, Application US/09579365

; Patent No. 6566585

; GENERAL INFORMATION:

; APPLICANT: Martin QUANZ

; TITLE OF INVENTION: GENETICALLY MODIFIED PLANT CELLS AND PLANTS WITH AN

; TITLE OF INVENTION: INCREASED ACTIVITY OF AN AMYLOSUCRASE PROTEIN AND A

; TITLE OF INVENTION: BRANCHING ENZYME

; FILE REFERENCE: 0147-0200P

; CURRENT APPLICATION NUMBER: US/09/579,365



; CURRENT FILING DATE: 2000-05-25  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 2475  
 ; TYPE: DNA  
 ; ORGANISM: Neisseria denitrificans  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (170)..(2458)  
 US-09-579-365-1

Query Match 100.0%; Score 2475; DB.3; Length 2475;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 1   | ACTGTATGCCGTGCAGCTGGAAAACCTGCTGGGCGTACGCGACAACCTCAATATTCCCGG  | 60  |
|    |     |   |     |
| Db | 1   | ACTGTATGCCGTGCAGCTGGAAAACCTGCTGGGCGTACGCGACAACCTCAATATTCCCGG  | 60  |
| Qy | 61  | CGTGGCCGAAGGCTATCCGAAGTGGGCGCGCAAATGCCGAGCCTCTGGAAGCCTTTGC    | 120 |
|    |     |   |     |
| Db | 61  | CGTGGCCGAAGGCTATCCGAAGTGGGCGCGCAAATGCCGAGCCTCTGGAAGCCTTTGC    | 120 |
| Qy | 121 | CCGCCACCCGCAAATGGGCAAGCAGCTTGCCATGATGGGAGACATCCGCATGAACCGAAA  | 180 |
|    |     |   |     |
| Db | 121 | CCGCCACCCGCAAATGGGCAAGCAGCTTGCCATGATGGGAGACATCCGCATGAACCGAAA  | 180 |
| Qy | 181 | CCGCCATATCCGACGCGGCTACCACCCGGAAGCCGAGAACGCCAAATCATCGACAGCCT   | 240 |
|    |     |   |     |
| Db | 181 | CCGCCATATCCGACGCGGCTACCACCCGGAAGCCGAGAACGCCAAATCATCGACAGCCT   | 240 |
| Qy | 241 | GTTTGCCGCCACCCACAGCGATCCGTTTGCCTATCTTGGGCGGCATCGTGTCAACGACGA  | 300 |
|    |     |   |     |
| Db | 241 | GTTTGCCGCCACCCACAGCGATCCGTTTGCCTATCTTGGGCGGCATCGTGTCAACGACGA  | 300 |
| Qy | 301 | ACGCGAAGCCGTGCGCGTGCTGCGTCCCGACGCGCACCATCGACATCATCGACCGCCA    | 360 |
|    |     |   |     |
| Db | 301 | ACGCGAAGCCGTGCGCGTGCTGCGTCCCGACGCGCACCATCGACATCATCGACCGCCA    | 360 |
| Qy | 361 | CACAGGCGCAGTCATCATGCCGTCTGAAAAATCGACGAGCGCGGCCTGTTTGCCGCCGT   | 420 |
|    |     |   |     |
| Db | 361 | CACAGGCGCAGTCATCATGCCGTCTGAAAAATCGACGAGCGCGGCCTGTTTGCCGCCGT   | 420 |
| Qy | 421 | ATTGCCCCGAACACGCGCCCGACTACGCCCTGCTGGTGACATACCACGAGGGCGAAGCCGC | 480 |
|    |     |   |     |
| Db | 421 | ATTGCCCCGAACACGCGCCCGACTACGCCCTGCTGGTGACATACCACGAGGGCGAAGCCGC | 480 |
| Qy | 481 | CGTACGCGAAGAAGATGACTACCGCTTCGGCAGCGCGCTGCAACATACCGATGCCTGGCT  | 540 |
|    |     |   |     |
| Db | 481 | CGTACGCGAAGAAGATGACTACCGCTTCGGCAGCGCGCTGCAACATACCGATGCCTGGCT  | 540 |
| Qy | 541 | GCTGGGCGAAGGCACGCACCTGCGCCCTTATGAAACGCTGGGCGCACATTTGCGCGAAAT  | 600 |
|    |     |   |     |
| Db | 541 | GCTGGGCGAAGGCACGCACCTGCGCCCTTATGAAACGCTGGGCGCACATTTGCGCGAAAT  | 600 |
| Qy | 601 | GGACGGCGTATCCGGCGTGCGCTTTGCCGTTTGGGCGCCCAACGCGCGGCGGGTATCGGT  | 660 |
|    |     |   |     |
| Db | 601 | GGACGGCGTATCCGGCGTGCGCTTTGCCGTTTGGGCGCCCAACGCGCGGCGGGTATCGGT  | 660 |
| Qy | 661 | CATCGGCGAATTCAACGGCTGGGACAGCCGCCCATGCCATGCGTCCGCACACAGGCAA    | 720 |

|    |      |  |      |
|----|------|--|------|
| Db | 661  | <br>CATCGGCGAATTCAACGGCTGGGACAGCCGCCCATGCCATGCGTCCGCACACAGGCAA     | 720  |
| Qy | 721  | CGGCCTGTGGGACATCTTTATCCCCGGCGTCGGCCTCAACGCGCTGTATAAATTCTCCGT       | 780  |
| Db | 721  | <br>CGGCCTGTGGGACATCTTTATCCCCGGCGTCGGCCTCAACGCGCTGTATAAATTCTCCGT   | 780  |
| Qy | 781  | ACTCGATGCCAACGGCAACATCCGCGAAAAAGCCGACCCCTACGCATTTCGGCGCGGAGCT      | 840  |
| Db | 781  | <br>ACTCGATGCCAACGGCAACATCCGCGAAAAAGCCGACCCCTACGCATTTCGGCGCGGAGCT  | 840  |
| Qy | 841  | GCGCCCGACCAACCGCATCCGTGGTGC GCGGCTTGCCGGCCAAAGCCGAAGCGCCGCTTT      | 900  |
| Db | 841  | <br>GCGCCCGACCAACCGCATCCGTGGTGC GCGGCTTGCCGGCCAAAGCCGAAGCGCCGCTTT  | 900  |
| Qy | 901  | CCGCCGCGCGCCAACCTCCGTGGAAGCGCCCATCAGCATTTACGAAGTCCATCTCGGCTC       | 960  |
| Db | 901  | <br>CCGCCGCGCGCCAACCTCCGTGGAAGCGCCCATCAGCATTTACGAAGTCCATCTCGGCTC   | 960  |
| Qy | 961  | GTGGCGGCGCAATCCCGAAAACAACACTACTGGCTCACCTACACGCAGCTGGCCGACGAATT     | 1020 |
| Db | 961  | <br>GTGGCGGCGCAATCCCGAAAACAACACTACTGGCTCACCTACACGCAGCTGGCCGACGAATT | 1020 |
| Qy | 1021 | GGTGAACATATGTAAAAGACATGGGCTTCACCCACATCGAGCTGCTGCCCTTGTCGAATA       | 1080 |
| Db | 1021 | <br>GGTGAACATATGTAAAAGACATGGGCTTCACCCACATCGAGCTGCTGCCCTTGTCGAATA   | 1080 |
| Qy | 1081 | TCCGTTTCGACGGCTCATGGGGCTACCAAGCCACCGGCCTGTATGCACCGACCAGCCGCTT      | 1140 |
| Db | 1081 | <br>TCCGTTTCGACGGCTCATGGGGCTACCAAGCCACCGGCCTGTATGCACCGACCAGCCGCTT  | 1140 |
| Qy | 1141 | CGGCTCGCCCGATGAGCTGAAAGCCCTGATTGACGCCGCCACGCCCGGCATCAGCGT          | 1200 |
| Db | 1141 | <br>CGGCTCGCCCGATGAGCTGAAAGCCCTGATTGACGCCGCCACGCCCGGCATCAGCGT      | 1200 |
| Qy | 1201 | GATTCTCGACTGGGTAGCGGGGCACTTCCCCACCGACGACCACGGCCTCAACACCTTCGA       | 1260 |
| Db | 1201 | <br>GATTCTCGACTGGGTAGCGGGGCACTTCCCCACCGACGACCACGGCCTCAACACCTTCGA   | 1260 |
| Qy | 1261 | CGGCACGGCGCTTTACGAACACGCCGACCCGCGCGAAGGCTACCATCAGGATTGGAACAC       | 1320 |
| Db | 1261 | <br>CGGCACGGCGCTTTACGAACACGCCGACCCGCGCGAAGGCTACCATCAGGATTGGAACAC   | 1320 |
| Qy | 1321 | GCTGATTTACAACCTTCGGCCGCAACGAAGTCAAAAACCTTCTGCAGGGCAACGCGCTCTA      | 1380 |
| Db | 1321 | <br>GCTGATTTACAACCTTCGGCCGCAACGAAGTCAAAAACCTTCTGCAGGGCAACGCGCTCTA  | 1380 |
| Qy | 1381 | CTGGATTGAGCGTTTCGGCTTCGACGGCATCCGCGTGGACGCCGTGGCCTCGATGATTTA       | 1440 |
| Db | 1381 | <br>CTGGATTGAGCGTTTCGGCTTCGACGGCATCCGCGTGGACGCCGTGGCCTCGATGATTTA   | 1440 |
| Qy | 1441 | CCGCAACTACTCGCGCAAAGACGGCGAGTGGATTCCCAACCGCTACGGCGGCAGCGAAAA       | 1500 |
| Db | 1441 | <br>CCGCAACTACTCGCGCAAAGACGGCGAGTGGATTCCCAACCGCTACGGCGGCAGCGAAAA   | 1500 |
| Qy | 1501 | TCTGGAAGCCATCGCCTTTTTGCGCCAAACCAATGCCGTCTTAAAAAGCGAAACACCCGG       | 1560 |
| Db | 1501 | <br>TCTGGAAGCCATCGCCTTTTTGCGCCAAACCAATGCCGTCTTAAAAAGCGAAACACCCGG   | 1560 |
| Qy | 1561 | CGCCGGCTCGTTTGCCGAAGAATCGACTTCCTTTGCCGACGTAACCCGCGAAGCCGGCCT       | 1620 |
|    |      |  |      |

## SCORE Search Results Details for Application 10705195 and Search Result us-10-705-195-1.rn

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments](#) / [Sugg](#)

This page gives you Search Results detail for the Application 10705195 and Search Result us-10-705-195-1.rn.pbm.

[start](#)

[Go Back to pre](#)

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 22, 2006, 19:27:25 ; Search time 2640 Seconds  
(without alignments)  
11519.658 Million cell updates/sec

Title: US-10-705-195-1  
Perfect score: 2475  
Sequence: 1 actgtatgccgtgcagctgg.....taaagcggcaccatactgcc 2475

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

## SUMMARIES

| Result | No. | Score | %<br>Query<br>Match | Length  | DB | ID                   | Description       |
|--------|-----|-------|---------------------|---------|----|----------------------|-------------------|
|        | 1   | 2475  | 100.0               | 2475    | 8  | US-10-705-195-1      | Sequence 1, Appli |
|        | 2   | 846   | 34.2                | 2187    | 7  | US-10-369-493-47275  | Sequence 47275, A |
|        | 3   | 844.4 | 34.1                | 2361    | 7  | US-10-336-753-35     | Sequence 35, Appl |
| c      | 4   | 789.8 | 31.9                | 908766  | 10 | US-10-795-159-685    | Sequence 685, App |
| c      | 5   | 779.8 | 31.5                | 6306    | 10 | US-10-795-159-510    | Sequence 510, App |
|        | 6   | 759.6 | 30.7                | 1830121 | 8  | US-10-329-670-1      | Sequence 1, Appli |
|        | 7   | 759.6 | 30.7                | 1830121 | 9  | US-10-158-865-1      | Sequence 1, Appli |
|        | 8   | 759.6 | 30.7                | 1830121 | 10 | US-10-981-687-1      | Sequence 1, Appli |
|        | 9   | 757.4 | 30.6                | 2193    | 8  | US-10-282-122A-22315 | Sequence 22315, A |
|        | 10  | 690.2 | 27.9                | 2151    | 7  | US-10-369-493-31456  | Sequence 31456, A |
|        | 11  | 680.6 | 27.5                | 2164    | 7  | US-10-369-493-44536  | Sequence 44536, A |
|        | 12  | 678.6 | 27.4                | 2199    | 8  | US-10-389-647-118    | Sequence 118, App |
|        | 13  | 663.6 | 26.8                | 2154    | 7  | US-10-369-493-39263  | Sequence 39263, A |
|        | 14  | 663   | 26.8                | 2160    | 7  | US-10-369-493-39639  | Sequence 39639, A |
|        | 15  | 663   | 26.8                | 2160    | 7  | US-10-369-493-40003  | Sequence 40003, A |
|        | 16  | 657   | 26.5                | 2079    | 10 | US-10-450-763-24644  | Sequence 24644, A |
|        | 17  | 647.4 | 26.2                | 2214    | 7  | US-10-369-493-35986  | Sequence 35986, A |
|        | 18  | 644.6 | 26.0                | 2163    | 7  | US-10-369-493-37808  | Sequence 37808, A |
|        | 19  | 639.8 | 25.9                | 2514    | 7  | US-10-156-761-2792   | Sequence 2792, Ap |
|        | 20  | 639.8 | 25.9                | 9025608 | 7  | US-10-156-761-1      | Sequence 1, Appli |
|        | 21  | 627.4 | 25.3                | 2142    | 7  | US-10-369-493-39258  | Sequence 39258, A |
|        | 22  | 627.4 | 25.3                | 2142    | 7  | US-10-369-493-39631  | Sequence 39631, A |
|        | 23  | 627.4 | 25.3                | 2142    | 7  | US-10-369-493-39999  | Sequence 39999, A |
|        | 24  | 617.2 | 24.9                | 2205    | 7  | US-10-369-493-42994  | Sequence 42994, A |
|        | 25  | 593.6 | 24.0                | 2148    | 7  | US-10-369-493-45400  | Sequence 45400, A |
|        | 26  | 591.4 | 23.9                | 1776    | 7  | US-10-156-761-7377   | Sequence 7377, Ap |
|        | 27  | 546.8 | 22.1                | 2118    | 7  | US-10-369-493-24319  | Sequence 24319, A |
|        | 28  | 546   | 22.1                | 1884    | 7  | US-10-369-493-32715  | Sequence 32715, A |
|        | 29  | 546   | 22.1                | 2034    | 7  | US-10-200-055-22     | Sequence 22, Appl |
|        | 30  | 537.6 | 21.7                | 2178    | 7  | US-10-369-493-43277  | Sequence 43277, A |
|        | 31  | 521.2 | 21.1                | 1434    | 10 | US-10-450-763-29239  | Sequence 29239, A |
| c      | 32  | 521.2 | 21.1                | 1434    | 10 | US-10-450-763-29661  | Sequence 29661, A |
|        | 33  | 512.2 | 20.7                | 2157    | 7  | US-10-369-493-33706  | Sequence 33706, A |
|        | 34  | 510.2 | 20.6                | 2256646 | 8  | US-10-470-565-1      | Sequence 1, Appli |
|        | 35  | 471.4 | 19.0                | 2268    | 7  | US-10-369-493-44638  | Sequence 44638, A |
|        | 36  | 443.4 | 17.9                | 2313    | 7  | US-10-369-493-26467  | Sequence 26467, A |
|        | 37  | 431   | 17.4                | 1893    | 7  | US-10-369-493-23737  | Sequence 23737, A |
|        | 38  | 430.8 | 17.4                | 2193    | 3  | US-09-738-626-1354   | Sequence 1354, Ap |
|        | 39  | 430.8 | 17.4                | 2316    | 9  | US-10-781-014-361    | Sequence 361, App |
| c      | 40  | 430.8 | 17.4                | 3309400 | 3  | US-09-738-626-1      | Sequence 1, Appli |
|        | 41  | 401   | 16.2                | 2250    | 7  | US-10-369-493-43535  | Sequence 43535, A |
|        | 42  | 348   | 14.1                | 1049    | 10 | US-10-450-763-24637  | Sequence 24637, A |
|        | 43  | 348   | 14.1                | 1049    | 10 | US-10-450-763-29235  | Sequence 29235, A |
|        | 44  | 348   | 14.1                | 1851    | 7  | US-10-369-493-33578  | Sequence 33578, A |
|        | 45  | 346.6 | 14.0                | 2340    | 10 | US-10-450-763-4093   | Sequence 4093, Ap |

## ALIGNMENTS

## RESULT 1

US-10-705-195-1

; Sequence 1, Application US/10705195

; Publication No. US20040110254A1

```

; GENERAL INFORMATION:
; APPLICANT: BUTTCHER, Volker et al.
; TITLE OF INVENTION: Method for producing alpha-1, 6-branched alpha-1, 4-glucans fro
; FILE REFERENCE: 0147-0253P
; CURRENT APPLICATION NUMBER: US/10/705,195
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 09/807,063
; PRIOR FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2475
; TYPE: DNA
; ORGANISM: Neisseria denitrificans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (170)..(2458)
US-10-705-195-1

```

```

Query Match          100.0%; Score 2475; DB 8; Length 2475;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 ACTGTATGCCGTGCAGCTGGAAAACCTGCTGGGCGTACGCGACAACCTCAATATTCCCGG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ACTGTATGCCGTGCAGCTGGAAAACCTGCTGGGCGTACGCGACAACCTCAATATTCCCGG 60

Qy     61 CGTGGCCGAAGGCTATCCGAACCTGGGCGCGCAAAATGCCGCGAGCCTCTGGAAGCCTTTGC 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CGTGGCCGAAGGCTATCCGAACCTGGGCGCGCAAAATGCCGCGAGCCTCTGGAAGCCTTTGC 120

Qy    121 CCGCCACCCGCAAATGGGCAAGCAGCTTGCCATGATGGGAGACATCCGCATGAACCGAAA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCGCCACCCGCAAATGGGCAAGCAGCTTGCCATGATGGGAGACATCCGCATGAACCGAAA 180

Qy    181 CCGCCATATCCGACGCGGCTACCACCCGGAAGCCGGAGAACGCCAAATCATCGACAGCCT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCGCCATATCCGACGCGGCTACCACCCGGAAGCCGGAGAACGCCAAATCATCGACAGCCT 240

Qy    241 GTTTGCCGCCACCCACAGCGATCCGTTTGCCTATCTTGGGCGGCATCGTGTCAACGACGA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTTTGCCGCCACCCACAGCGATCCGTTTGCCTATCTTGGGCGGCATCGTGTCAACGACGA 300

Qy    301 ACGCGAAGCCGTGCGCGTGCTGCGTCCCGACGCGCACCACATCGACATCATCGACCGCCA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ACGCGAAGCCGTGCGCGTGCTGCGTCCCGACGCGCACCACATCGACATCATCGACCGCCA 360

Qy    361 CACAGGCGCAGTCATCATGCCGTCTGAAAAAATCGACGAGCGCGGCCTGTTTGCCGCCGT 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CACAGGCGCAGTCATCATGCCGTCTGAAAAAATCGACGAGCGCGGCCTGTTTGCCGCCGT 420

Qy    421 ATTGCCCCGAACACGCGCCCGACTACGCCCTGCTGGTGACATACCACGAGGGCGAAGCCGC 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ATTGCCCCGAACACGCGCCCGACTACGCCCTGCTGGTGACATACCACGAGGGCGAAGCCGC 480

Qy    481 CGTACGCGAAGAAGATGACTACCGCTTCGGCAGCGCGCTGCAACATACCGATGCCTGGCT 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CGTACGCGAAGAAGATGACTACCGCTTCGGCAGCGCGCTGCAACATACCGATGCCTGGCT 540

Qy    541 GCTGGGCGAAGGCACGCACCTGCGCCCTTATGAAACGCTGGGCGCACATTTCCGCCGAAAT 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```

|    |      |  |      |
|----|------|--|------|
| Db | 541  | GCTGGGCGAAGGCACGCACCTGCGCCCTTATGAAACGCTGGGCGCACATTTGCGCGAAAT   | 600  |
| Qy | 601  | GGACGGCGTATCCGGCGTGCGCTTTGCCGTTTGGGCGCCCAACGCGCGGCGGGTATCGGT   | 660  |
|    |      |  |      |
| Db | 601  | GGACGGCGTATCCGGCGTGCGCTTTGCCGTTTGGGCGCCCAACGCGCGGCGGGTATCGGT   | 660  |
| Qy | 661  | CATCGGCGAATTCAACGGCTGGGACAGCCGCCCATGCCATGCGTCCGCACACAGGCAA     | 720  |
|    |      |  |      |
| Db | 661  | CATCGGCGAATTCAACGGCTGGGACAGCCGCCCATGCCATGCGTCCGCACACAGGCAA     | 720  |
| Qy | 721  | CGGCCTGTGGGACATCTTTATCCCCGGCGTCGGCCTCAACGCGCTGTATAAATTCTCCGT   | 780  |
|    |      |  |      |
| Db | 721  | CGGCCTGTGGGACATCTTTATCCCCGGCGTCGGCCTCAACGCGCTGTATAAATTCTCCGT   | 780  |
| Qy | 781  | ACTCGATGCCAACGGCAACATCCGCGAAAAAGCCGACCCCTACGCATTTCGGCGCGGAGCT  | 840  |
|    |      |  |      |
| Db | 781  | ACTCGATGCCAACGGCAACATCCGCGAAAAAGCCGACCCCTACGCATTTCGGCGCGGAGCT  | 840  |
| Qy | 841  | GCGCCCGACCACCGCATCCGTGGTGCGCGGCTTGCCGGCCAAAGCCGAAGCGCCGCTTT    | 900  |
|    |      |  |      |
| Db | 841  | GCGCCCGACCACCGCATCCGTGGTGCGCGGCTTGCCGGCCAAAGCCGAAGCGCCGCTTT    | 900  |
| Qy | 901  | CCGCCCGCGCGCCAACTCCGTGGAAGCGCCCATCAGCATTTACGAAGTCCATCTCGGCTC   | 960  |
|    |      |  |      |
| Db | 901  | CCGCCCGCGCGCCAACTCCGTGGAAGCGCCCATCAGCATTTACGAAGTCCATCTCGGCTC   | 960  |
| Qy | 961  | GTGGCGGCGCAATCCCGAAAACAATACTGGCTCACCTACACGCAGCTGGCCGACGAATT    | 1020 |
|    |      |  |      |
| Db | 961  | GTGGCGGCGCAATCCCGAAAACAATACTGGCTCACCTACACGCAGCTGGCCGACGAATT    | 1020 |
| Qy | 1021 | GGTGAACATATGTAAAAGACATGGGCTTCACCCACATCGAGCTGCTGCCCTTGTCCGAATA  | 1080 |
|    |      |  |      |
| Db | 1021 | GGTGAACATATGTAAAAGACATGGGCTTCACCCACATCGAGCTGCTGCCCTTGTCCGAATA  | 1080 |
| Qy | 1081 | TCCGTTTCGACGGCTCATGGGGCTACCAAGCCACCGGCCTGTATGCACCGACCAGCCGCTT  | 1140 |
|    |      |  |      |
| Db | 1081 | TCCGTTTCGACGGCTCATGGGGCTACCAAGCCACCGGCCTGTATGCACCGACCAGCCGCTT  | 1140 |
| Qy | 1141 | CGGCTCGCCCGATGAGCTGAAAGCCCTGATTGACGCCGCCACGCCGCCGGCATCAGCGT    | 1200 |
|    |      |  |      |
| Db | 1141 | CGGCTCGCCCGATGAGCTGAAAGCCCTGATTGACGCCGCCACGCCGCCGGCATCAGCGT    | 1200 |
| Qy | 1201 | GATTCTCGACTGGGTAGCGGGGCACTTCCCCACCGACGACCACGGCCTCAACACCTTCGA   | 1260 |
|    |      |  |      |
| Db | 1201 | GATTCTCGACTGGGTAGCGGGGCACTTCCCCACCGACGACCACGGCCTCAACACCTTCGA   | 1260 |
| Qy | 1261 | CGGCACGGCGCTTTACGAACACGCCGACCCGCGCGAAGGCTACCATCAGGATTGGAACAC   | 1320 |
|    |      |  |      |
| Db | 1261 | CGGCACGGCGCTTTACGAACACGCCGACCCGCGCGAAGGCTACCATCAGGATTGGAACAC   | 1320 |
| Qy | 1321 | GCTGATTTACAACCTTCGGCCGCAACGAAGTCAAAAACCTTCCTGCAGGGCAACGCGCTCTA | 1380 |
|    |      |  |      |
| Db | 1321 | GCTGATTTACAACCTTCGGCCGCAACGAAGTCAAAAACCTTCCTGCAGGGCAACGCGCTCTA | 1380 |
| Qy | 1381 | CTGGATTGAGCGTTTCGGCTTCGACGGCATCCGCGTGGACGCCGTGGCCTCGATGATTTA   | 1440 |
|    |      |  |      |
| Db | 1381 | CTGGATTGAGCGTTTCGGCTTCGACGGCATCCGCGTGGACGCCGTGGCCTCGATGATTTA   | 1440 |
| Qy | 1441 | CCGCAACTACTCGCGCAAAGACGGCGAGTGGATTCCCAACCGCTACGGCGGCAGCGAAAA   | 1500 |
|    |      |  |      |
| Db | 1441 | CCGCAACTACTCGCGCAAAGACGGCGAGTGGATTCCCAACCGCTACGGCGGCAGCGAAAA   | 1500 |

# SCORE Search Results Details for Application 10705195 and Search Result us-10-705-195-1.rnpbn

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments](#) / [Suggest](#)

This page gives you Search Results detail for the Application 10705195 and Search Result us-10-705-195-1.rnpbn.

[start](#)

[Go Back to](#)

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 22, 2006, 19:30:46 ; Search time 399 Seconds  
(without alignments)  
9915.919 Million cell updates/sec

Title: US-10-705-195-1  
Perfect score: 2475  
Sequence: 1 actgtatgccgtgcagctgg.....taaagcggcaccatactgcc 2475

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA\_New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq1:\*  
9: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq2:\*  
10: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|----|-------------|
|------------|-------|--------------------|----|-------------|

|     |       |      |      |   |                       |                   |
|-----|-------|------|------|---|-----------------------|-------------------|
| 1   | 846   | 34.2 | 2187 | 9 | US-11-275-569-17      | Sequence 17, Appl |
| 2   | 844.4 | 34.1 | 2361 | 9 | US-11-330-822-38      | Sequence 38, Appl |
| 3   | 180.8 | 7.3  | 1869 | 9 | US-11-348-413-6911    | Sequence 6911, Ap |
| 4   | 142   | 5.7  | 3553 | 6 | US-10-449-902-12839   | Sequence 12839, A |
| 5   | 95    | 3.8  | 640  | 8 | US-11-266-748A-119619 | Sequence 119619,  |
| c 6 | 95    | 3.8  | 641  | 8 | US-11-266-748A-81241  | Sequence 81241, A |
| 7   | 95    | 3.8  | 641  | 8 | US-11-266-748A-134052 | Sequence 134052,  |
| 8   | 75.6  | 3.1  | 2668 | 9 | US-11-056-355B-76595  | Sequence 76595, A |
| 9   | 75.4  | 3.0  | 2891 | 8 | US-11-266-748A-25857  | Sequence 25857, A |
| 10  | 74    | 3.0  | 2763 | 9 | US-11-056-355B-99154  | Sequence 99154, A |
| 11  | 74    | 3.0  | 2763 | 9 | US-11-056-355B-110393 | Sequence 110393,  |
| 12  | 74    | 3.0  | 2764 | 6 | US-10-953-349-4536    | Sequence 4536, Ap |
| 13  | 74    | 3.0  | 2764 | 9 | US-11-056-355B-27071  | Sequence 27071, A |
| 14  | 74    | 3.0  | 2764 | 9 | US-11-056-355B-30239  | Sequence 30239, A |
| 15  | 74    | 3.0  | 2764 | 9 | US-11-056-355B-33829  | Sequence 33829, A |
| 16  | 65.8  | 2.7  | 3643 | 8 | US-11-216-545-3261    | Sequence 3261, Ap |
| 17  | 65    | 2.6  | 2588 | 9 | US-11-056-355B-100250 | Sequence 100250,  |
| 18  | 65    | 2.6  | 2588 | 9 | US-11-056-355B-111489 | Sequence 111489,  |
| 19  | 62.2  | 2.5  | 1350 | 9 | US-11-316-535A-11     | Sequence 11, Appl |
| 20  | 62.2  | 2.5  | 1761 | 9 | US-11-316-535A-176    | Sequence 176, App |
| 21  | 61.8  | 2.5  | 2763 | 9 | US-11-056-355B-19641  | Sequence 19641, A |
| 22  | 61.8  | 2.5  | 2763 | 9 | US-11-056-355B-19806  | Sequence 19806, A |
| 23  | 61.8  | 2.5  | 2826 | 9 | US-11-218-305-12549   | Sequence 12549, A |
| 24  | 60.2  | 2.4  | 2115 | 8 | US-11-217-529-698     | Sequence 698, App |
| 25  | 60    | 2.4  | 2649 | 6 | US-10-539-723-6       | Sequence 6, Appli |
| 26  | 58    | 2.3  | 1309 | 6 | US-10-449-902-20908   | Sequence 20908, A |
| 27  | 57.4  | 2.3  | 2115 | 8 | US-11-217-529-76256   | Sequence 76256, A |
| 28  | 57    | 2.3  | 1338 | 9 | US-11-316-535A-21     | Sequence 21, Appl |
| 29  | 54.2  | 2.2  | 1323 | 9 | US-11-316-535A-39     | Sequence 39, Appl |
| 30  | 52.6  | 2.1  | 1118 | 8 | US-11-266-748A-228183 | Sequence 228183,  |
| 31  | 52.4  | 2.1  | 3932 | 9 | US-11-218-305-13556   | Sequence 13556, A |
| 32  | 52    | 2.1  | 1338 | 9 | US-11-316-535A-130    | Sequence 130, App |
| 33  | 51.2  | 2.1  | 1312 | 6 | US-10-449-902-26592   | Sequence 26592, A |
| 34  | 51.2  | 2.1  | 1365 | 6 | US-10-449-902-7232    | Sequence 7232, Ap |
| 35  | 50.8  | 2.1  | 1347 | 9 | US-11-056-355B-12252  | Sequence 12252, A |
| 36  | 50.8  | 2.1  | 2640 | 9 | US-11-330-822-58      | Sequence 58, Appl |
| 37  | 50.8  | 2.1  | 2759 | 9 | US-11-218-305-12548   | Sequence 12548, A |
| 38  | 50.6  | 2.0  | 1707 | 6 | US-10-449-902-23277   | Sequence 23277, A |
| 39  | 50.4  | 2.0  | 2226 | 9 | US-11-218-305-13555   | Sequence 13555, A |
| 40  | 50    | 2.0  | 1616 | 9 | US-11-218-305-3848    | Sequence 3848, Ap |
| 41  | 49.6  | 2.0  | 1296 | 6 | US-10-449-902-27170   | Sequence 27170, A |
| 42  | 49.6  | 2.0  | 1345 | 6 | US-10-449-902-23472   | Sequence 23472, A |
| 43  | 49.6  | 2.0  | 1462 | 6 | US-10-449-902-1135    | Sequence 1135, Ap |
| 44  | 49.6  | 2.0  | 2127 | 6 | US-10-449-902-10143   | Sequence 10143, A |
| 45  | 48.6  | 2.0  | 1436 | 9 | US-11-174-307B-4393   | Sequence 4393, Ap |

## ALIGNMENTS

## RESULT 1

US-11-275-569-17

; Sequence 17, Application US/11275569

; Publication No. US20060160192A1

; GENERAL INFORMATION:

; APPLICANT: Ajinomoto Co., Inc.

; TITLE OF INVENTION: METHOD FOR PRODUCING L-AMINO ACID USING BACTERIUM OF THE

; TITLE OF INVENTION: ENTEROBACTERIACEAE FAMILY HAVING PATHWAY OF GLYCOGEN BIOSYNTHETIC

; FILE REFERENCE: C440-C5323

; CURRENT APPLICATION NUMBER: US/11/275,569



```
; CURRENT FILING DATE: 2006-01-17
; PRIOR APPLICATION NUMBER: RU2005101110
; PRIOR FILING DATE: 2005-01-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 2187
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2187)
US-11-275-569-17
```

```
Query Match          34.2%; Score 846; DB 9; Length 2187;
Best Local Similarity 62.6%; Pred. No. 5.9e-206;
Matches 1358; Conservative 0; Mismatches 800; Indels 12; Gaps 2;
```

```
Qy      218 GAACGCCAAATCATCGACAGCCTGTTTGCCGCCACCCACAGCGATCCGTTTGCCTATCTT 277
      || | | | | | | | | | | | | | | | | | | | | | |
Db      16 GATAGAGACGTGATTAACGCGCTAATTCAGGCCATTTTGC GGATCCTTTTCCGTACTG 75

Qy      278 GGGCGGCATCGTGTCAACGACGAACGCGAAGCCGTGCGCGTGCTGCGTCCCGACGCGCAC 337
      || | | | | | | | | | | | | | | | | | | | | | |
Db      76 GGAATGCATAAAACCACCGCGGGACTGGAAG---TCCGTGCCCTTTTACCCGACGCTACC 132

Qy      338 CACATCGACATCATCGACCGCCACACAGGCGCAGTCATCATGCCGTCTGAAAAAATCGAC 397
      | | | | | | | | | | | | | | | | | | | | | |
Db      133 GATGTGTGGGTGATTGAACCGAAAACCGGGCGCAAACCTCGCAAACCTGGAGTGTCTCGAC 192

Qy      398 GAGCGCGGCCTGTTTGCCGCCGTATTGCCCGAACACGCGCCCGACTACGCCCTGCTGGTG 457
      || | | | | | | | | | | | | | | | | | | | | | |
Db      193 TCACGGGGATTCTTTAGCGGCGTCATTCCGCGACGTAAGAATTTTTTCCGCTATCAGTTG 252

Qy      458 ACATACCACGAGGGCGAAGCCGCCGTACGCGAAGAAGATGACTACCGCTTCGGCAGCGCG 517
      | | | | | | | | | | | | | | | | | | | | | |
Db      253 GCTGTTGTCTGGCATGGTCAGCAAAACCTGATTGATGATCCTTACCGTTTTGGTCCGCTA 312

Qy      518 CTGCAACATAACCGATGCCTGGCTGCTGGGCGAAGGCACGCACCTGCGCCCTTATGAAACG 577
      | | | | | | | | | | | | | | | | | | | | | |
Db      313 ATCCAGGAAATGGATGCCTGGCTATTATCTGAAGGTACTCACCTGCGCCCGTATGAAACC 372

Qy      578 CTGGGCGCACATTTCCGCCAAATGGACGGCGTATCCGGCGTGCGCTTTGCCGTTTGGGCG 637
      | | | | | | | | | | | | | | | | | | | | | |
Db      373 TTAGGCGCGCATGCAGATACTATGGATGGCGTCACAGGTACGCGTTTCTCTGTCTGGGCT 432

Qy      638 CCCAACGCGCGCGGGGTATCGGTCATCGGCGAATTCAACGGCTGGGACAGCCGCCGCCAT 697
      || | | | | | | | | | | | | | | | | | | | | | |
Db      433 CCAAACGCCCCTCGGGTCTCGGTGGTTGGGCAATTCAACTACTGGGACGGTCGCCGTCAC 492

Qy      698 GCCATGCGTCCGCACACAGGCAACGGCCTGTGGGACATCTTTATCCCCGGCGTCGGCCTC 757
      | | | | | | | | | | | | | | | | | | | | | |
Db      493 CCGATGCGCCTGCGTAAAGAGAGCGGCATCTGGGAAGTGTATCCCTGGGGCGCATAAC 552

Qy      758 AACGCGCTGTATAAATTCTCCGTACTCGATGCCAACGGCAACATCCGCGAAAAAGCCGAC 817
      || | | | | | | | | | | | | | | | | | | | | | |
Db      553 GGTCAGCTCTATAAATACGAGATGATTGATGCCAATGGCAACTTGCGTCTGAAGTCCGAC 612

Qy      818 CCCTACGCATTTCGGCGCGGAGCTGCGCCCGACCACCGCATCCGTGGTGCGCGGCTTGCCG 877
      || | | | | | | | | | | | | | | | | | | | | | |
Db      613 CCTTATGCCTTTGAAGCGCAAATGCGCCCGGAAACCGCGTCTCTTATTTGCGGGCTGCCG 672
```

|    |      |   |      |
|----|------|---|------|
| Qy | 878  | GCCAAAGCCGAAGCGCCGCTTTCCGCCGCCGCGCCAACTCCGTGGAAGCGCCCATCAGC   | 937  |
|    |      |   |      |
| Db | 673  | GAAAAGGTTGTACAGACTGAAGAGCGCAAAAAGCGAATCAGTTTGATGCGCCAATCTCT   | 732  |
| Qy | 938  | ATTTACGAAGTCCATCTCGGCTCGTGGCGGCGCAATCCCGAAAACAATACTGGCTCACC   | 997  |
|    |      |   |      |
| Db | 733  | ATTTATGAAGTTCACCTGGGTTCTCGGCTCGCCACACCGACAACAATTTCTGGTTGAGC   | 792  |
| Qy | 998  | TACACGCAGCTGGCCGACGAATTGGTGAATATGTAAAAGACATGGGCTTCACCCACATC   | 1057 |
|    |      |   |      |
| Db | 793  | TACCGCGAGCTGGCCGATCAACTGGTGCCTTATGCTAAATGGATGGGCTTTACCCACCTC  | 852  |
| Qy | 1058 | GAGCTGCTGCCCTTGTCCGAATATCCGTTTCGACGGCTCATGGGGCTACCAAGCCACCGGC | 1117 |
|    |      |   |      |
| Db | 853  | GAATACTGCCCATTAAACGAGCATCCCTTCGATGGCAGTTGGGGTTATCAGCCAACCGGC  | 912  |
| Qy | 1118 | CTGTATGCACCGACCAGCCGCTTCGGCTCGCCCGATGAGCTGAAAGCCCTGATTGACGCC  | 1177 |
|    |      |   |      |
| Db | 913  | CTGTATGCGCCAACCCGCCGTTTTGGTACTCGCGACGACTTCCGTTATTTTCATTGATGCC | 972  |
| Qy | 1178 | GCCACGCGCCCGGCATCAGCGTGATTCTCGACTGGGTAGCGGGGCACTTCCCCACCGAC   | 1237 |
|    |      |   |      |
| Db | 973  | GCACACGCAGCTGGTCTGAACGTGATTCTCGACTGGGTGCCAGGCCACTTCCCGACTGAT  | 1032 |
| Qy | 1238 | GACCACGGCCTCAACACCTTCGACGGCACGGCGCTTTACGAACACGCCGACCCGCGCGAA  | 1297 |
|    |      |   |      |
| Db | 1033 | GACTTTGCGCTTGCCGAATTTGATGGCACGAATTTGTATGAACACAGCGATCCGCGTGAA  | 1092 |
| Qy | 1298 | GGCTACCATCAGGATTGGAACACGCTGATTTACAATTCGGCCGCAACGAAGTCAAAAAC   | 1357 |
|    |      |   |      |
| Db | 1093 | GGCTATCATCAGGACTGGAACACGCTGATCTACAATATGGTCGCCGTGAAGTCAGTAA    | 1152 |
| Qy | 1358 | TTCCTGCAGGGCAACGCGCTCTACTGGATTGAGCGTTTCGGCTTCGACGGCATCCGCGTG  | 1417 |
|    |      |   |      |
| Db | 1153 | TTCCTCGTCGGTAACGCGCTTTACTGGATTGAACGTTTTGGTATTGATGCGCTGCGCGTC  | 1212 |
| Qy | 1418 | GACGCCGTGGCCTCGATGATTTACCGCAACTACTCGCGCAAAGACGGCGAGTGGATTCCC  | 1477 |
|    |      |   |      |
| Db | 1213 | GATGCGGTGGCGTCAATGATTTATCGCGACTACAGCCGTAAAGAGGGGGAGTGGATCCCG  | 1272 |
| Qy | 1478 | AACCGCTACGGCGGCAGCGAAAATCTGGAAGCCATCGCCTTTTTGCGCCAAACCAATGCC  | 1537 |
|    |      |   |      |
| Db | 1273 | AACGAATTTGGCGGGCGCGAGAATCTGAAGCGATTGAATTCTTGCGTAATACCAACCGT   | 1332 |
| Qy | 1538 | GTCTTAAAAAGCGAAACACCCGGCGCGGCTCGTTTTGCCGAAGAATCGACTTCCTTTGCC  | 1597 |
|    |      |   |      |
| Db | 1333 | ATTCTTGGTGAGCAGTTTCCGGTGCGGTGACAATGGCTGAGGAGTCTACCGATTTCCT    | 1392 |
| Qy | 1598 | GACGTAACCCG-----CGAAGCCGGCCTGAACTTCGATTTCAAATGGAATATGGGC      | 1648 |
|    |      |   |      |
| Db | 1393 | GGCGTTTCTCGTCCGAGGATATGGGCGGTCTGGGCTTCTGGTACAAGTGAACCTCGGC    | 1452 |
| Qy | 1649 | TGGATGAACGACACCCTGCGCTATATGCAGGAAGACCCCGTCCACCGCAAATACCACCAC  | 1708 |
|    |      |   |      |
| Db | 1453 | TGGATGCATGACACCCTGGACTACATGAAGCTCGACCCGGTTTATCGTCAGTATCATCAC  | 1512 |
| Qy | 1709 | GGCAAAATGACATTCCGGCATGATGTACCAATACAGCGAAAATTCGTTCTGCCCTGTGCG  | 1768 |
|    |      |   |      |
| Db | 1513 | GATAAACTGACCTTCGGGATTCTCTACAACTACACTGAAAATTCGTCCTGCCGTTGTGCG  | 1572 |

# SCORE Search Results Details for Application

## 2.p2r

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 10705195 and Search Result us-10-705-1...  
[start](#)

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 22, 2006, 19:34:08 ; Search time 11195 Seconds  
(without alignments)  
6528.977 Million cell updates/sec

Title: US-10-705-195-2  
Perfect score: 4112  
Sequence: 1 MNRNRHIRRGYHPEAGERQI.....QTALRADKQPAVKDKQAKAK 762

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+\_p2n.model -DEV=xlh  
-Q=/abss/ABSSWEB\_spool/US10705195/runat\_22082006\_095549\_849/app\_query.fasta\_1  
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss04  
-USER=US10705195 @CGN\_1\_1\_7218 @runat\_22082006\_095549\_849 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:\*  
1: gb\_env:\*  
2: gb\_pat:\*  
3: gb\_ph:\*  
4: gb\_pl:\*  
5: gb\_pr:\*

6: gb\_ro:\*  
 7: gb\_sts:\*  
 8: gb\_sy:\*  
 9: gb\_un:\*  
 10: gb\_vi:\*  
 11: gb\_ov:\*  
 12: gb\_htg:\*  
 13: gb\_in:\*  
 14: gb\_om:\*  
 15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result | %   |        |             |        |                | Description        |
|--------|-----|--------|-------------|--------|----------------|--------------------|
|        | No. | Score  | Query Match | Length | ID             |                    |
|        | 1   | 4112   | 100.0       | 2475   | 2 BD236814     | BD236814 Nucleic a |
|        | 2   | 4112   | 100.0       | 2475   | 2 AR337816     | AR337816 Sequence  |
|        | 3   | 4112   | 100.0       | 2475   | 2 AR479077     | AR479077 Sequence  |
|        | 4   | 4112   | 100.0       | 2475   | 2 AX055494     | AX055494 Sequence  |
|        | 5   | 4112   | 100.0       | 2475   | 15 AF102867    | AF102867 Neisseria |
| c      | 6   | 2570   | 62.5        | 110000 | 15 AE016827_11 | Continuation (12 o |
|        | 7   | 2568.5 | 62.5        | 12519  | 15 AE006089    | AE006089 Pasteurel |
|        | 8   | 2533   | 61.6        | 2307   | 2 AR387231     | AR387231 Sequence  |
| c      | 9   | 2531   | 61.6        | 110000 | 15 CP000057_16 | Continuation (17 o |
| c      | 10  | 2531   | 61.6        | 349980 | 2 CQ873160     | CQ873160 Sequence  |
|        | 11  | 2526   | 61.4        | 110000 | 2 BD426631_14  | Continuation (15 o |
|        | 12  | 2526   | 61.4        | 110000 | 2 AR274513_14  | Continuation (15 o |
|        | 13  | 2526   | 61.4        | 110000 | 2 AR632719_14  | Continuation (15 o |
|        | 14  | 2525   | 61.4        | 110000 | 15 L42023_14   | Continuation (15 o |
| c      | 15  | 2481.5 | 60.3        | 6306   | 2 CQ872897     | CQ872897 Sequence  |
| c      | 16  | 2475.5 | 60.2        | 110000 | 15 AE017220_36 | Continuation (37 o |
|        | 17  | 2472.5 | 60.1        | 110000 | 15 AE014613_41 | Continuation (42 o |
|        | 18  | 2472.5 | 60.1        | 265050 | 15 AL627281    | AL627281 Salmonell |
| c      | 19  | 2471.5 | 60.1        | 23506  | 15 AE008863    | AE008863 Salmonell |
| c      | 20  | 2471.5 | 60.1        | 110000 | 15 CP000026_34 | Continuation (35 o |
| c      | 21  | 2469.5 | 60.1        | 110000 | 15 AE014075_39 | Continuation (40 o |
| c      | 22  | 2469.5 | 60.1        | 110000 | 15 AE014075_40 | Continuation (41 o |
| c      | 23  | 2467.5 | 60.0        | 110000 | 15 AE005174_43 | Continuation (44 o |
| c      | 24  | 2467.5 | 60.0        | 110000 | 15 BA000007_42 | Continuation (43 o |
| c      | 25  | 2465.5 | 60.0        | 110000 | 15 AE005674_35 | Continuation (36 o |
|        | 26  | 2465.5 | 60.0        | 110000 | 15 AE014073_42 | Continuation (43 o |
|        | 27  | 2462.5 | 59.9        | 2361   | 2 BD071178     | BD071178 Plant lik |
|        | 28  | 2462.5 | 59.9        | 2559   | 15 ECOGLGBA    | M13751 Escherichia |
| c      | 29  | 2462.5 | 59.9        | 110000 | 15 U00096_35   | Continuation (36 o |
|        | 30  | 2462.5 | 59.9        | 110000 | 15 AP009048_40 | Continuation (41 o |
| c      | 31  | 2462.5 | 59.9        | 110000 | 15 CP000038_38 | Continuation (39 o |
| c      | 32  | 2457.5 | 59.8        | 72438  | 15 ECOUW67_3   | Continuation (4 of |
|        | 33  | 2456.5 | 59.7        | 2055   | 2 CS221362     | CS221362 Sequence  |
| c      | 34  | 2456.5 | 59.7        | 110000 | 15 CP000034_33 | Continuation (34 o |
| c      | 35  | 2454.5 | 59.7        | 110000 | 15 CP000036_34 | Continuation (35 o |
|        | 36  | 2438   | 59.3        | 12144  | 15 AE013993    | AE013993 Yersinia  |
| c      | 37  | 2438   | 59.3        | 110000 | 15 BX936398_44 | Continuation (45 o |
| c      | 38  | 2438   | 59.3        | 199050 | 15 AJ414159    | AJ414159 Yersinia  |
| c      | 39  | 2438   | 59.3        | 294253 | 15 AE017139    | AE017139 Yersinia  |
| c      | 40  | 2435.5 | 59.2        | 110000 | 15 BX950851_46 | Continuation (47 o |
|        | 41  | 2430   | 59.1        | 2520   | 15 AF434710    | AF434710 Pectobact |

|   |    |        |      |        |    |             |                    |
|---|----|--------|------|--------|----|-------------|--------------------|
| c | 42 | 2239   | 54.5 | 110000 | 15 | BX936398_45 | Continuation (46 o |
|   | 43 | 2068.5 | 50.3 | 110000 | 15 | CP000230_29 | Continuation (30 o |
|   | 44 | 2040.5 | 49.6 | 348068 | 15 | BX572604    | BX572604 Rhodopseu |
| c | 45 | 2035.5 | 49.5 | 110000 | 15 | AP007255_33 | Continuation (34 o |

## ALIGNMENTS

## RESULT 1

BD236814

LOCUS BD236814 2475 bp DNA linear PAT 17-JUL-2003

DEFINITION Nucleic acid molecule encoding branching enzyme from *Neisseria* bacteria and process for producing alpha-1,6-branched alpha-1,4-glucane.

ACCESSION BD236814

VERSION BD236814.1 GI:33046584

KEYWORDS JP 2002527068-A/1.

SOURCE *Bergeriella denitrificans*ORGANISM *Bergeriella denitrificans*Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; *Bergeriella*.

REFERENCE 1 (bases 1 to 2475)

AUTHORS Buttcher,V. and Quanz,M.

TITLE Nucleic acid molecule encoding branching enzyme from *Neisseria* bacteria and process for producing alpha-1,6-branchedJOURNAL Patent: JP 2002527068-A 1 27-AUG-2002;  
PLANTTEC BIOTECHNOLOGIE GMBH FORSCHUNG UND ENTWICKLUNG, MAX PLANCK  
GESELLSCHAFT ZUR FOERDERUNG DER WISSENSCHAFTEN EVCOMMENT OS *Neisseria denitrificans*

PN JP 2002527068-A/1

PD 27-AUG-2002

PF 08-OCT-1999 JP 2000576030

PR 09-OCT-1998 DE 198 46 635.8,27-MAY-1999 DE 199 24 342.5 PI

VOLKER BUTTCHER,MARTIN QUANZ.

PC C12N15/09,A01H5/00,C07K16/40,C12N1/15,C12N1/19,C12N1/21,C12N5/

PC 10,C12N9/10,

PC C12P19/04,C12N15/00,C12N5/00

CC Nucleic acid molecule encoding branching  
enzyme from *Neisseria*

CC bacteria

CC and process for producing alpha-1,6-branched alpha-1,4-glucane

FH Key Location/Qualifiers

FT CDS (170)..(2458).

FEATURES Location/Qualifiers

source 1..2475

/organism="*Bergeriella denitrificans*"

/mol\_type="genomic DNA"

/db\_xref="taxon:494"

## ORIGIN

## Alignment Scores:

|                        |         |               |      |
|------------------------|---------|---------------|------|
| Pred. No.:             | 0       | Length:       | 2475 |
| Score:                 | 4112.00 | Matches:      | 762  |
| Percent Similarity:    | 100.0%  | Conservative: | 0    |
| Best Local Similarity: | 100.0%  | Mismatches:   | 0    |
| Query Match:           | 100.0%  | Indels:       | 0    |
| DB:                    | 2       | Gaps:         | 0    |

US-10-705-195-2 (1-762) x BD236814 (1-2475)

Qy 1 MetAsnArgAsnArgHisIleArgArgGlyTyrHisProGluAlaGlyGluArgGlnIle 20

|    |      |   |      |
|----|------|---|------|
| Db | 170  | <br>ATGAACCGAAACCGCCATATCCGACGCGGCTACCACCCGGAAGCCGGAGAACGCCAAATC  | 229  |
| Qy | 21   | IleAspSerLeuPheAlaAlaThrHisSerAspProPheAlaTyrLeuGlyArgHisArg      | 40   |
| Db | 230  | <br>ATCGACAGCCTGTTTGGCGCCACCCACAGCGATCCGTTTGCCTATCTTGGGCGGCATCGT  | 289  |
| Qy | 41   | ValAsnAspGluArgGluAlaValArgValLeuArgProAspAlaHisHisIleAspIle      | 60   |
| Db | 290  | <br>GTCAACGACGAACGCGAAGCCGTGCGCGTGCTGCGTCCCGACGCGCACCACATCGACATC  | 349  |
| Qy | 61   | IleAspArgHisThrGlyAlaValIleMetProSerGluLysIleAspGluArgGlyLeu      | 80   |
| Db | 350  | <br>ATCGACCGCCACACAGGCGCAGTCATCATGCCGTCTGAAAAATCGACGAGCGCGGCCTG   | 409  |
| Qy | 81   | PheAlaAlaValLeuProGluHisAlaProAspTyrAlaLeuLeuValThrTyrHisGlu      | 100  |
| Db | 410  | <br>TTTGCCGCCGTATTGCCCGAACACGCGCCCGACTACGCCCTGCTGGTGACATACCACGAG  | 469  |
| Qy | 101  | GlyGluAlaAlaValArgGluGluAspAspTyrArgPheGlySerAlaLeuGlnHisThr      | 120  |
| Db | 470  | <br>GGCGAAGCCGCCGTACGCGAAGAAGATGACTACCGCTTCGGCAGCGCGCTGCAACATACC  | 529  |
| Qy | 121  | AspAlaTrpLeuLeuGlyGluGlyThrHisLeuArgProTyrGluThrLeuGlyAlaHis      | 140  |
| Db | 530  | <br>GATGCCTGGCTGCTGGGCGAAGGCACGCACCTGCGCCCTTATGAAACGCTGGGCGCACAT  | 589  |
| Qy | 141  | PheAlaGluMetAspGlyValSerGlyValArgPheAlaValTrpAlaProAsnAlaArg      | 160  |
| Db | 590  | <br>TTCGCCGAAATGGACGGCGTATCCGGCGTGCGCTTTGCCGTTGGGCGCCCAACGCGCGG   | 649  |
| Qy | 161  | ArgValSerValIleGlyGluPheAsnGlyTrpAspSerArgArgHisAlaMetArgPro      | 180  |
| Db | 650  | <br>CGGGTATCGGTCATCGGCGAATTCAACGGCTGGGACAGCCGCCCATGCCATGCGTCCG    | 709  |
| Qy | 181  | HisThrGlyAsnGlyLeuTrpAspIlePheIleProGlyValGlyLeuAsnAlaLeuTyr      | 200  |
| Db | 710  | <br>CACACAGGCAACGGCCTGTGGGACATCTTTATCCCCGGCGTGGCCTCAACGCGCTGTAT   | 769  |
| Qy | 201  | LysPheSerValLeuAspAlaAsnGlyAsnIleArgGluLysAlaAspProTyrAlaPhe      | 220  |
| Db | 770  | <br>AAATTCTCCGTACTCGATGCCAACGGCAACATCCGCGAAAAAGCCGACCCCTACGCATTC  | 829  |
| Qy | 221  | GlyAlaGluLeuArgProThrThrAlaSerValValArgGlyLeuProAlaLysAlaGlu      | 240  |
| Db | 830  | <br>GGCGCGGAGCTGCGCCCGACCACCGCATCCGTGGTGCGCGGCTTGCCGGCCAAAGCCGAA  | 889  |
| Qy | 241  | AlaProAlaPheArgArgArgAlaAsnSerValGluAlaProIleSerIleTyrGluVal      | 260  |
| Db | 890  | <br>GCGCCCGCTTTCCGCCGCGCGCCAACCTCCGTGGAAGCGCCCATCAGCATTTACGAAGTC  | 949  |
| Qy | 261  | HisLeuGlySerTrpArgArgAsnProGluAsnAsnTyrTrpLeuThrTyrThrGlnLeu      | 280  |
| Db | 950  | <br>CATCTCGGCTCGTGGCGGCGCAATCCCGAAAAACAATACTGGGCTCACCTACACGCAGCTG | 1009 |
| Qy | 281  | AlaAspGluLeuValAsnTyrValLysAspMetGlyPheThrHisIleGluLeuLeuPro      | 300  |
| Db | 1010 | <br>GCCGACGAATTGGTGAACATGTAAAAGACATGGGCTTCACCCACATCGAGCTGCTGCC    | 1069 |
| Qy | 301  | LeuSerGluTyrProPheAspGlySerTrpGlyTyrGlnAlaThrGlyLeuTyrAlaPro      | 320  |
|    |      |   |      |

## SCORE Search Results Details for Application 107 Search Result us-10-705-195-2.p2n.rng

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments](#) / [Sugg](#)

This page gives you Search Results detail for the Application 10705195 and Search Result us-10-705-195-2.p2n.rng  
[start](#)

[Go](#)

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 22, 2006, 19:33:36 ; Search time 1177 Seconds  
(without alignments)  
6770.841 Million cell updates/sec

Title: US-10-705-195-2  
Perfect score: 4112  
Sequence: 1 MNRNRHIRRGYHPEAGERQI.....QTALRADKQPAVKDKQAKAK 762

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/abss/ABSSWEB\_spool/US10705195/runat\_22082006\_095547\_838/app\_query.fasta\_1  
-DB=N\_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss08  
-USER=US10705195\_CGN\_1\_1\_786 @runat\_22082006\_095547\_838 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_8:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*

6: geneseqn2002as:\*  
 7: geneseqn2002bs:\*  
 8: geneseqn2003as:\*  
 9: geneseqn2003bs:\*  
 10: geneseqn2003cs:\*  
 11: geneseqn2003ds:\*  
 12: geneseqn2004as:\*  
 13: geneseqn2004bs:\*  
 14: geneseqn2005s:\*  
 15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result | No. | Score  | %<br>Query Match | Length | DB | ID          | Description        |
|--------|-----|--------|------------------|--------|----|-------------|--------------------|
|        | 1   | 4112   | 100.0            | 2475   | 3  | AAA11731    | Aa11731 N. denitr  |
|        | 2   | 2533   | 61.6             | 2307   | 11 | ACH98165    | Ach98165 Klebsiell |
| c      | 3   | 2531   | 61.6             | 349980 | 13 | ADT05737    | Adt05737 Haemophil |
|        | 4   | 2526   | 61.4             | 110000 | 2  | AAT42063_14 | Continuation (15 o |
|        | 5   | 2523   | 61.4             | 2193   | 8  | ACA34445    | Aca34445 Prokaryot |
| c      | 6   | 2481.5 | 60.3             | 6306   | 13 | ADT05474    | Adt05474 Haemophil |
|        | 7   | 2462.5 | 59.9             | 2361   | 2  | AAV70952    | Aav70952 DNA seque |
|        | 8   | 2462   | 59.9             | 2187   | 13 | ADT48837    | Adt48837 Bacterial |
|        | 9   | 2038.5 | 49.6             | 2164   | 13 | ADT46098    | Adt46098 Bacterial |
|        | 10  | 1996   | 48.5             | 2151   | 13 | ADS55782    | Ads55782 Bacterial |
|        | 11  | 1957.5 | 47.6             | 2148   | 13 | ADT46962    | Adt46962 Bacterial |
|        | 12  | 1939   | 47.2             | 2079   | 5  | AAS88840    | Aas88840 DNA encod |
|        | 13  | 1925.5 | 46.8             | 2154   | 13 | ADS63589    | Ads63589 Bacterial |
|        | 14  | 1925.5 | 46.8             | 2160   | 13 | ADS63965    | Ads63965 Bacterial |
|        | 15  | 1925.5 | 46.8             | 2160   | 13 | ADT41565    | Adt41565 Bacterial |
|        | 16  | 1910   | 46.4             | 2163   | 13 | ADS62134    | Ads62134 Bacterial |
|        | 17  | 1899.5 | 46.2             | 2214   | 13 | ADS60312    | Ads60312 Bacterial |
|        | 18  | 1887   | 45.9             | 2331   | 6  | ABQ90257    | Abq90257 M. capsul |
|        | 19  | 1859   | 45.2             | 2199   | 13 | ADS14563    | Ads14563 Pseudomon |
|        | 20  | 1840   | 44.7             | 2472   | 11 | ABD09593    | Abd09593 Pseudomon |
|        | 21  | 1828.5 | 44.5             | 2142   | 13 | ADS63957    | Ads63957 Bacterial |
|        | 22  | 1828.5 | 44.5             | 2142   | 13 | ADS64325    | Ads64325 Bacterial |
|        | 23  | 1828.5 | 44.5             | 2142   | 13 | ADS63584    | Ads63584 Bacterial |
|        | 24  | 1812.5 | 44.1             | 2178   | 13 | ADT44839    | Adt44839 Bacterial |
| c      | 25  | 1808   | 44.0             | 11276  | 14 | ACL64571    | ACL64571 M. xanthu |
|        | 26  | 1805   | 43.9             | 2172   | 14 | ACL68441    | ACL68441 M. xanthu |
|        | 27  | 1805   | 43.9             | 2205   | 13 | ADT44556    | Adt44556 Bacterial |
|        | 28  | 1791   | 43.6             | 2157   | 13 | ADS58032    | Ads58032 Bacterial |
|        | 29  | 1766   | 42.9             | 2034   | 10 | ADG18862    | Adg18862 DNA encod |
|        | 30  | 1760   | 42.8             | 1884   | 13 | ADS57041    | Ads57041 Bacterial |
|        | 31  | 1756   | 42.7             | 2193   | 8  | ACF39411    | Acf39411 Mycobacte |
| c      | 32  | 1756   | 42.7             | 110000 | 4  | AAI99682_14 | Continuation (15 o |
|        | 33  | 1746.5 | 42.5             | 2313   | 13 | ADS48037    | Ads48037 Bacterial |
|        | 34  | 1732.5 | 42.1             | 2250   | 13 | ADT45097    | Adt45097 Bacterial |
| c      | 35  | 1727   | 42.0             | 110000 | 4  | AAI99683_14 | Continuation (15 o |
|        | 36  | 1700   | 41.3             | 1893   | 10 | ADC23310    | Adc23310 DNA of Aq |
|        | 37  | 1700   | 41.3             | 1893   | 13 | ADS45307    | Ads45307 Bacterial |
|        | 38  | 1684   | 41.0             | 2268   | 13 | ADT46200    | Adt46200 Bacterial |
|        | 39  | 1657.5 | 40.3             | 22934  | 4  | AAS59613    | Aas59613 Propionib |
|        | 40  | 1657.5 | 40.3             | 22934  | 8  | ACF64542    | Acf64542 Propionib |
|        | 41  | 1649   | 40.1             | 349980 | 6  | ABQ81846    | Abq81846 Bifidobac |



|      |        |      |        |   |          |                    |
|------|--------|------|--------|---|----------|--------------------|
| 42   | 1649   | 40.1 | 349980 | 6 | ABQ81847 | Abq81847 Bifidobac |
| 43   | 1626.5 | 39.6 | 2193   | 5 | AAH66319 | Aah66319 C glutami |
| 44   | 1626.5 | 39.6 | 2316   | 4 | AAF71540 | Aaf71540 Corynebac |
| c 45 | 1626.5 | 39.6 | 349980 | 5 | AAH68528 | Aah68528 C glutami |

## ALIGNMENTS

## RESULT 1

AAA11731

ID AAA11731 standard; DNA; 2475 BP.

XX

AC AAA11731;

XX

DT 21-JUL-2000 (first entry)

XX

DE N. denitrificans alpha-1,6-branched alpha-1,4 glucan DNA.

XX

KW Alpha-1,6-branched alpha-1,4-glucan; branching enzyme; binder; carrier;

KW transgenic plant; flavor; perfume; packaging material; papermaking;

KW ultra-violet light adsorber; starch; textile; wetting agent; ds.

XX

OS Neisseria denitrificans.

XX

FH Key Location/Qualifiers

FT CDS 170. .2458

FT /\*tag= a

FT /product= "alpha-1,6-branched alpha-1,4-glucan"

XX

PN WO200022140-A1.

XX

PD 20-APR-2000.

XX

PF 08-OCT-1999; 99WO-EP007562.

XX

PR 09-OCT-1998; 98DE-01046635.

PR 27-MAY-1999; 99DE-01024342.

XX

PA (PLAN-) PLANTTEC BIOTECHNOLOGIE GMBH.

PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX

PI Buettcher V, Quanz M;

XX

DR WPI; 2000-317992/27.

DR P-PSDB; AAW90977.

XX

PT New nucleic acid encoding a branching enzyme, useful for in vitro

PT synthesis of branched glucans and to prepare transgenic plants producing

PT modified starch.

XX

PS Claim 1b; Page 93-96; 115pp; German.

XX

CC This invention describes a novel nucleic acid (I) isolated from Neisseria

CC which encodes a branching enzyme (II). (I) is used for recombinant

CC production of (II) subsequently used in the in vitro production of alpha-

CC 1,6-branched alpha-1,4-glucans. It is also used to prepare transgenic

CC plants that produce starches with modified properties. (III) are used as

CC binders for tablets, carriers for pharmaceuticals, flavors and perfumes

CC and powdered additives, packaging materials, ultra-violet light adsorbers

CC in sunscreens and also for any of the usual applications of starch in

CC foods, papermaking, as textile size, in soil stabilization, as wetting

CC agent for agricultural chemicals, as polymer additives etc. Fragments of  
 CC (I) are useful as PCR primers and antisense molecules or ribozymes for  
 CC inhibiting expression of (I), and the regulatory region of (II) can be  
 CC used to control expression of heterologous sequences in host cells. (I)  
 CC provides an inexpensive method for producing alpha-1,6-branched alpha-1,4  
 CC -glucans (III), producing products that can be tailored for particular  
 CC applications, particularly by controlling the degree of branching. Starch  
 CC from transgenic plants has increased gel strength; reduced phosphate  
 CC content; reduced peak viscosity; lower pasting temperature and granule  
 CC size and/or altered sidechain distribution. This sequence encodes an  
 CC alpha-1,6-branched alpha-1,4-glucan isolated from *Neisseria denitrificans*  
 CC which is described in the method of the invention

XX

SQ Sequence 2475 BP; 560 A; 827 C; 674 G; 414 T; 0 U; 0 Other;

#### Alignment Scores:

|                        |         |               |      |
|------------------------|---------|---------------|------|
| Pred. No.:             | 0       | Length:       | 2475 |
| Score:                 | 4112.00 | Matches:      | 762  |
| Percent Similarity:    | 100.0%  | Conservative: | 0    |
| Best Local Similarity: | 100.0%  | Mismatches:   | 0    |
| Query Match:           | 100.0%  | Indels:       | 0    |
| DB:                    | 3       | Gaps:         | 0    |

US-10-705-195-2. (1-762) x AAA11731 (1-2475)

|    |     |  |     |
|----|-----|--|-----|
| Qy | 1   | MetAsnArgAsnArgHisIleArgArgGlyTyrHisProGluAlaGlyGluArgGlnIle | 20  |
| Db | 170 | ATGAACCGAAACCGCCATATCCGACGCGGTACCACCCGGAAGCCGGAGAACGCCAAATC  | 229 |
| Qy | 21  | IleAspSerLeuPheAlaAlaThrHisSerAspProPheAlaTyrLeuGlyArgHisArg | 40  |
| Db | 230 | ATCGACAGCCTGTTTGCCGCCACCCACAGCGATCCGTTTGCCTATCTTGGGCGGCATCGT | 289 |
| Qy | 41  | ValAsnAspGluArgGluAlaValArgValLeuArgProAspAlaHisHisIleAspIle | 60  |
| Db | 290 | GTCAACGACGAACGCGAAGCCGTGCGCGTGCTGCGTCCCGACGCGCACCACATCGACATC | 349 |
| Qy | 61  | IleAspArgHisThrGlyAlaValIleMetProSerGluLysIleAspGluArgGlyLeu | 80  |
| Db | 350 | ATCGACCGCCACACAGGCGCAGTCATCATGCCGTCTGAAAAAATCGACGAGCGCGGCCTG | 409 |
| Qy | 81  | PheAlaAlaValLeuProGluHisAlaProAspTyrAlaLeuLeuValThrTyrHisGlu | 100 |
| Db | 410 | TTTGCCGCGGTATTGCCCGAACACGCGCCCGACTACGCCCTGCTGGTGACATACCACGAG | 469 |
| Qy | 101 | GlyGluAlaAlaValArgGluGluAspAspTyrArgPheGlySerAlaLeuGlnHisThr | 120 |
| Db | 470 | GGCGAAGCCGCGGTACGCGAAGAAGATGACTACCGCTTCGGCAGCGCGCTGCAACATACC | 529 |
| Qy | 121 | AspAlaTrpLeuLeuGlyGluGlyThrHisLeuArgProTyrGluThrLeuGlyAlaHis | 140 |
| Db | 530 | GATGCCTGGCTGCTGGGCGAAGGCACGCACCTGCGCCCTTATGAAACGCTGGGCGCACAT | 589 |
| Qy | 141 | PheAlaGluMetAspGlyValSerGlyValArgPheAlaValTrpAlaProAsnAlaArg | 160 |
| Db | 590 | TTGCCCGAAATGGACGGCGTATCCGGCGTGCGCTTGCCGTTTGGGCGCCCAACGCGCGG  | 649 |
| Qy | 161 | ArgValSerValIleGlyGluPheAsnGlyTrpAspSerArgArgHisAlaMetArgPro | 180 |
| Db | 650 | CGGGTATCGGTCATCGGCGAATTCAACGGCTGGGACAGCCGCGCCATGCCATGCGTCCG  | 709 |

## SCORE Search Results Details for Application 10705195 and Search Result us-10-705-195-2.p2n.rni

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10705195 and Search Result us-10-705-195-2.p2n.rni.

[start](#)

[Go Back to](#)

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 22, 2006, 19:40:37 ; Search time 360 Seconds  
(without alignments)  
5940.770 Million cell updates/sec

Title: US-10-705-195-2  
Perfect score: 4112  
Sequence: 1 MNRNRHIRRGYHPEAGERQI.....QTALRADKQPAVKDKQAKAK 762

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+\_p2n.model -DEV=xlh  
-Q=/abss/ABSSWEB\_spool/US10705195/runat\_22082006\_095553\_938/app\_query.fasta\_1  
-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-HOST=abss05h -USER=US10705195\_CGN\_1\_1\_211@runat\_22082006\_095553\_938 -NCPUs=6  
-ICPU=3 -NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA:  
1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*  
 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*  
 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*  
 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result |     |        | %     |         |    |                     | ID | Description       |
|--------|-----|--------|-------|---------|----|---------------------|----|-------------------|
|        | No. | Score  | Match | Length  | DB |                     |    |                   |
|        | 1   | 4112   | 100.0 | 2475    | 3  | US-09-579-365-1     |    | Sequence 1, Appli |
|        | 2   | 4112   | 100.0 | 2475    | 3  | US-09-807-063-1     |    | Sequence 1, Appli |
|        | 3   | 2533   | 61.6  | 2307    | 3  | US-09-489-039A-3960 |    | Sequence 3960, Ap |
|        | 4   | 2526   | 61.4  | 1830121 | 3  | US-09-557-884-1     |    | Sequence 1, Appli |
|        | 5   | 2526   | 61.4  | 1830121 | 3  | US-09-643-990A-1    |    | Sequence 1, Appli |
|        | 6   | 2526   | 61.4  | 1830121 | 3  | US-10-158-865-1     |    | Sequence 1, Appli |
|        | 7   | 1840   | 44.7  | 2472    | 3  | US-09-252-991A-8197 |    | Sequence 8197, Ap |
| c      | 8   | 1808   | 44.0  | 11276   | 3  | US-09-902-540-1034  |    | Sequence 1034, Ap |
|        | 9   | 1805   | 43.9  | 2172    | 3  | US-09-902-540-4904  |    | Sequence 4904, Ap |
| c      | 10  | 1756   | 42.7  | 4411529 | 3  | US-09-103-840A-1    |    | Sequence 1, Appli |
| c      | 11  | 1727   | 42.0  | 4403765 | 3  | US-09-103-840A-2    |    | Sequence 2, Appli |
|        | 12  | 1541   | 37.5  | 1866    | 3  | US-09-537-120-1     |    | Sequence 1, Appli |
| c      | 13  | 1465   | 35.6  | 1230025 | 3  | US-09-198-452A-1    |    | Sequence 1, Appli |
| c      | 14  | 1465   | 35.6  | 1230230 | 3  | US-09-438-185A-1    |    | Sequence 1, Appli |
|        | 15  | 1422.5 | 34.6  | 2426    | 3  | US-08-528-026C-3    |    | Sequence 3, Appli |
| c      | 16  | 1387   | 33.7  | 1701    | 3  | US-09-252-991A-8109 |    | Sequence 8109, Ap |
|        | 17  | 1387   | 33.7  | 1877    | 5  | US-09-974-300-653   |    | Sequence 653, App |
|        | 18  | 1216.5 | 29.6  | 1956    | 3  | US-09-107-433-242   |    | Sequence 242, App |
|        | 19  | 1216   | 29.6  | 1929    | 3  | US-09-583-110-1148  |    | Sequence 1148, Ap |
| c      | 20  | 1179.5 | 28.7  | 11384   | 3  | US-08-961-527-45    |    | Sequence 45, Appl |
|        | 21  | 1179   | 28.7  | 36470   | 3  | US-08-311-731A-123  |    | Sequence 123, App |
|        | 22  | 1012.5 | 24.6  | 1308    | 3  | US-09-252-991A-8131 |    | Sequence 8131, Ap |
|        | 23  | 729.5  | 17.7  | 976     | 3  | US-08-961-083-79    |    | Sequence 79, Appl |
|        | 24  | 729.5  | 17.7  | 976     | 3  | US-09-536-784-79    |    | Sequence 79, Appl |
|        | 25  | 729.5  | 17.7  | 976     | 3  | US-09-765-271-79    |    | Sequence 79, Appl |
|        | 26  | 729.5  | 17.7  | 976     | 3  | US-09-765-272A-79   |    | Sequence 79, Appl |
|        | 27  | 617    | 15.0  | 807     | 3  | US-09-634-238-168   |    | Sequence 168, App |
|        | 28  | 602.5  | 14.7  | 780     | 3  | US-09-902-540-2210  |    | Sequence 2210, Ap |
| c      | 29  | 602.5  | 14.7  | 781     | 3  | US-09-902-540-1586  |    | Sequence 1586, Ap |
|        | 30  | 601.5  | 14.6  | 2853    | 3  | US-09-609-040-3     |    | Sequence 3, Appli |
|        | 31  | 596.5  | 14.5  | 2665    | 3  | US-09-257-894-1     |    | Sequence 1, Appli |
|        | 32  | 596    | 14.5  | 2720    | 3  | US-09-731-166-11    |    | Sequence 11, Appl |
|        | 33  | 595    | 14.5  | 2578    | 3  | US-08-945-722-19    |    | Sequence 19, Appl |
|        | 34  | 595    | 14.5  | 2578    | 4  | US-10-056-454B-19   |    | Sequence 19, Appl |
|        | 35  | 592.5  | 14.4  | 2446    | 3  | US-09-731-166-9     |    | Sequence 9, Appli |
|        | 36  | 592    | 14.4  | 2529    | 3  | US-08-945-722-17    |    | Sequence 17, Appl |
|        | 37  | 592    | 14.4  | 2529    | 4  | US-10-056-454B-17   |    | Sequence 17, Appl |
|        | 38  | 590    | 14.3  | 3128    | 3  | US-08-716-449-1     |    | Sequence 1, Appli |
|        | 39  | 589.5  | 14.3  | 2531    | 4  | US-10-056-454B-37   |    | Sequence 37, Appl |
|        | 40  | 588.5  | 14.3  | 2554    | 5  | US-10-162-948-1     |    | Sequence 1, Appli |
|        | 41  | 588.5  | 14.3  | 2576    | 3  | US-08-945-722-16    |    | Sequence 16, Appl |
|        | 42  | 588.5  | 14.3  | 2576    | 4  | US-10-056-454B-16   |    | Sequence 16, Appl |
|        | 43  | 587    | 14.3  | 2725    | 3  | US-08-941-445A-14   |    | Sequence 14, Appl |
|        | 44  | 587    | 14.3  | 3074    | 3  | US-09-087-277-1     |    | Sequence 1, Appli |
|        | 45  | 587    | 14.3  | 3074    | 3  | US-09-658-499-1     |    | Sequence 1, Appli |

## ALIGNMENTS

## RESULT 1

US-09-579-365-1

; Sequence 1, Application US/09579365

; Patent No. 6566585

; GENERAL INFORMATION:

; APPLICANT: Martin QUANZ

; TITLE OF INVENTION: GENETICALLY MODIFIED PLANT CELLS AND PLANTS WITH AN

; TITLE OF INVENTION: INCREASED ACTIVITY OF AN AMYLOSUCRASE PROTEIN AND A

; TITLE OF INVENTION: BRANCHING ENZYME

; FILE REFERENCE: 0147-0200P

; CURRENT APPLICATION NUMBER: US/09/579,365

; CURRENT FILING DATE: 2000-05-25

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 2475

; TYPE: DNA

; ORGANISM: Neisseria denitrificans

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (170)..(2458)

US-09-579-365-1

## Alignment Scores:

|                        |         |               |      |
|------------------------|---------|---------------|------|
| Pred. No.:             | 0       | Length:       | 2475 |
| Score:                 | 4112.00 | Matches:      | 762  |
| Percent Similarity:    | 100.0%  | Conservative: | 0    |
| Best Local Similarity: | 100.0%  | Mismatches:   | 0    |
| Query Match:           | 100.0%  | Indels:       | 0    |
| DB:                    | 3       | Gaps:         | 0    |

US-10-705-195-2 (1-762) x US-09-579-365-1 (1-2475)

|    |     |  |     |
|----|-----|--|-----|
| Qy | 1   | MetAsnArgAsnArgHisIleArgArgGlyTyrHisProGluAlaGlyGluArgGlnIle | 20  |
| Db | 170 | ATGAACCGAAACCGCCATATCCGACGCGGTACACCCGGAAGCCGGAACGCCAAATC     | 229 |
| Qy | 21  | IleAspSerLeuPheAlaAlaThrHisSerAspProPheAlaTyrLeuGlyArgHisArg | 40  |
| Db | 230 | ATCGACAGCCTGTTTGCCGCCACCCACAGCGATCCGTTTGCCTATCTTGGGCGGCATCGT | 289 |
| Qy | 41  | ValAsnAspGluArgGluAlaValArgValLeuArgProAspAlaHisHisIleAspIle | 60  |
| Db | 290 | GTCAACGACGAACGCGAAGCCGTGCGCGTGCTGCGTCCCGACGCGCACCACATCGACATC | 349 |
| Qy | 61  | IleAspArgHisThrGlyAlaValIleMetProSerGluLysIleAspGluArgGlyLeu | 80  |
| Db | 350 | ATCGACCGCCACACAGGCGCAGTCATCATGCCGTCTGAAAAATCGACGAGCGCGGCCCTG | 409 |
| Qy | 81  | PheAlaAlaValLeuProGluHisAlaProAspTyrAlaLeuLeuValThrTyrHisGlu | 100 |
| Db | 410 | TTTGCCGCGGTATTGCCCGAACACGCGCCCGACTACGCCCTGCTGGTGACATACCACGAG | 469 |
| Qy | 101 | GlyGluAlaAlaValArgGluGluAspAspTyrArgPheGlySerAlaLeuGlnHisThr | 120 |
| Db | 470 | GGCGAAGCCGCCGTACGCGAAGAAGATGACTACCGCTTCGGCAGCGCGCTGCAACATACC | 529 |

|    |      |  |      |
|----|------|--|------|
| Qy | 121  | AspAlaTrpLeuLeuGlyGluGlyThrHisLeuArgProTyrGluThrLeuGlyAlaHis   | 140  |
|    |      |  |      |
| Db | 530  | GATGCCTGGCTGCTGGGCGAAGGCACGCACCTGCGCCCTTATGAAACGCTGGGCGCACAT   | 589  |
| Qy | 141  | PheAlaGluMetAspGlyValSerGlyValArgPheAlaValTrpAlaProAsnAlaArg   | 160  |
|    |      |  |      |
| Db | 590  | TTGCCCGAAATGGACGGCGTATCCGGCGTGCGCTTTGCCGTTTGGGCGCCCAACGCGCGG   | 649  |
| Qy | 161  | ArgValSerValIleGlyGluPheAsnGlyTrpAspSerArgArgHisAlaMetArgPro   | 180  |
|    |      |  |      |
| Db | 650  | CGGGTATCGGTCATCGGCGAATTCAACGGCTGGGACAGCCGCCCATGCCATGCGTCCG     | 709  |
| Qy | 181  | HisThrGlyAsnGlyLeuTrpAspIlePheIleProGlyValGlyLeuAsnAlaLeuTyr   | 200  |
|    |      |  |      |
| Db | 710  | CACACAGGCAACGGCCTGTGGGACATCTTTATCCCCGGCGTCGGCCTCAACGCGCTGTAT   | 769  |
| Qy | 201  | LysPheSerValLeuAspAlaAsnGlyAsnIleArgGluLysAlaAspProTyrAlaPhe   | 220  |
|    |      |  |      |
| Db | 770  | AAATTCTCCGTACTCGATGCCAACGGCAACATCCGCGAAAAAGCCGACCCCTACGCATTC   | 829  |
| Qy | 221  | GlyAlaGluLeuArgProThrThrAlaSerValValArgGlyLeuProAlaLysAlaGlu   | 240  |
|    |      |  |      |
| Db | 830  | GGCGCGGAGCTGCGCCCGACCACGCATCCGTGGTGCGCGGCTTGCCGGCCAAAGCCGAA    | 889  |
| Qy | 241  | AlaProAlaPheArgArgArgAlaAsnSerValGluAlaProIleSerIleTyrGluVal   | 260  |
|    |      |  |      |
| Db | 890  | GCGCCCGCTTTCCGCCGCCGCGCCAACTCCGTGGAAGCGCCCATCAGCATTTACGAAGTC   | 949  |
| Qy | 261  | HisLeuGlySerTrpArgArgAsnProGluAsnAsnTyrTrpLeuThrTyrThrGlnLeu   | 280  |
|    |      |  |      |
| Db | 950  | CATCTCGGCTCGTGGCGGCGCAATCCCGAAAACAATACTGGCTCACCTACACGCAGCTG    | 1009 |
| Qy | 281  | AlaAspGluLeuValAsnTyrValLysAspMetGlyPheThrHisIleGluLeuLeuPro   | 300  |
|    |      |  |      |
| Db | 1010 | GCCGACGAATTGGTGAACATATGTAAAGACATGGGCTTCACCCACATCGAGCTGCTGCCC   | 1069 |
| Qy | 301  | LeuSerGluTyrProPheAspGlySerTrpGlyTyrGlnAlaThrGlyLeuTyrAlaPro   | 320  |
|    |      |  |      |
| Db | 1070 | TTGTCCGAATATCCGTTTCGACGGCTCATGGGGCTACCAAGCCACCGGCCTGTATGCACCG  | 1129 |
| Qy | 321  | ThrSerArgPheGlySerProAspGluLeuLysAlaLeuIleAspAlaAlaHisAlaAla   | 340  |
|    |      |  |      |
| Db | 1130 | ACCAGCCGCTTCGGCTCGCCCGATGAGCTGAAAGCCCTGATTGACGCCGCCACGCCGCC    | 1189 |
| Qy | 341  | GlyIleSerValIleLeuAspTrpValAlaGlyHisPheProThrAspAspHisGlyLeu   | 360  |
|    |      |  |      |
| Db | 1190 | GGCATCAGCGTGATTCTCGACTGGGTAGCGGGGCACTTCCCCACCGACGACCACGGCCTC   | 1249 |
| Qy | 361  | AsnThrPheAspGlyThrAlaLeuTyrGluHisAlaAspProArgGluGlyTyrHisGln   | 380  |
|    |      |  |      |
| Db | 1250 | AACACCTTCGACGGCACGGCGCTTTACGAACACGCCGACCCGCGCGAAGGCTACCATCAG   | 1309 |
| Qy | 381  | AspTrpAsnThrLeuIleTyrAsnPheGlyArgAsnGluValLysAsnPheLeuGlnGly   | 400  |
|    |      |  |      |
| Db | 1310 | GATTGGAACACGCTGATTTACAACCTTCGGCCGCAACGAAGTCAAAAACCTTCCTGCAGGGC | 1369 |
| Qy | 401  | AsnAlaLeuTyrTrpIleGluArgPheGlyPheAspGlyIleArgValAspAlaValAla   | 420  |
|    |      |  |      |
| Db | 1370 | AACGCGCTCTACTGGATTGAGCGTTTCGGCTTCGACGGCATCCGCGTGGACGCCGTGGCC   | 1429 |
| Qy | 421  | SerMetIleTyrArgAsnTyrSerArgLysAspGlyGluTrpIleProAsnArgTyrGly   | 440  |

## SCORE Search Results Details for Application 10705195 and Search Result us-10-705-195-2.p2n.rnp1

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10705195 and Search Result us-10-705-195-2.p2n.rnp1.

[start](#)

[Go Back to Application List](#)

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 22, 2006, 19:56:13 ; Search time 495 Seconds  
(without alignments)  
3691.235 Million cell updates/sec

Title: US-10-705-195-2  
Perfect score: 4112  
Sequence: 1 MNRNRHIRRGYHPEAGERQI.....QTALRADKQPAVKDKQAKAK 762

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+\_p2n.model -DEV=xlh  
-Q=/abss/ABSSWEB\_spool/US10705195/runat\_22082006\_095558\_1059/app\_query.fasta\_1  
-DB=Published\_Applications\_NA\_New -QFMT=fastap -SUFFIX=p2n.rnp1 -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abss04  
-USER=US10705195\_CGN\_1\_1\_209\_@runat\_22082006\_095558\_1059 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_NA\_New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*

4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq1:\*  
 9: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq2:\*  
 10: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result | %   |        | Query |        |    |                       | Description       |
|--------|-----|--------|-------|--------|----|-----------------------|-------------------|
|        | No. | Score  | Match | Length | DB | ID                    |                   |
|        | 1   | 2462.5 | 59.9  | 2361   | 9  | US-11-330-822-38      | Sequence 38, Appl |
|        | 2   | 2462   | 59.9  | 2187   | 9  | US-11-275-569-17      | Sequence 17, Appl |
|        | 3   | 1224.5 | 29.8  | 1869   | 9  | US-11-348-413-6911    | Sequence 6911, Ap |
|        | 4   | 618.5  | 15.0  | 2668   | 9  | US-11-056-355B-76595  | Sequence 76595, A |
|        | 5   | 614.5  | 14.9  | 2763   | 9  | US-11-056-355B-99154  | Sequence 99154, A |
|        | 6   | 614.5  | 14.9  | 2763   | 9  | US-11-056-355B-110393 | Sequence 110393,  |
|        | 7   | 614.5  | 14.9  | 2764   | 6  | US-10-953-349-4536    | Sequence 4536, Ap |
|        | 8   | 614.5  | 14.9  | 2764   | 9  | US-11-056-355B-27071  | Sequence 27071, A |
|        | 9   | 614.5  | 14.9  | 2764   | 9  | US-11-056-355B-30239  | Sequence 30239, A |
|        | 10  | 614.5  | 14.9  | 2764   | 9  | US-11-056-355B-33829  | Sequence 33829, A |
|        | 11  | 604.5  | 14.7  | 3643   | 8  | US-11-216-545-3261    | Sequence 3261, Ap |
|        | 12  | 598    | 14.5  | 2588   | 9  | US-11-056-355B-100250 | Sequence 100250,  |
|        | 13  | 598    | 14.5  | 2588   | 9  | US-11-056-355B-111489 | Sequence 111489,  |
|        | 14  | 593    | 14.4  | 2759   | 9  | US-11-218-305-12548   | Sequence 12548, A |
|        | 15  | 592.5  | 14.4  | 2763   | 9  | US-11-056-355B-19641  | Sequence 19641, A |
|        | 16  | 592.5  | 14.4  | 2763   | 9  | US-11-056-355B-19806  | Sequence 19806, A |
|        | 17  | 592.5  | 14.4  | 2826   | 9  | US-11-218-305-12549   | Sequence 12549, A |
|        | 18  | 587    | 14.3  | 2640   | 9  | US-11-330-822-58      | Sequence 58, Appl |
|        | 19  | 569    | 13.8  | 3553   | 6  | US-10-449-902-12839   | Sequence 12839, A |
|        | 20  | 566    | 13.8  | 2649   | 6  | US-10-539-723-6       | Sequence 6, Appli |
|        | 21  | 547.5  | 13.3  | 2763   | 9  | US-11-330-822-60      | Sequence 60, Appl |
|        | 22  | 547.5  | 13.3  | 2790   | 9  | US-11-056-355B-11438  | Sequence 11438, A |
|        | 23  | 547.5  | 13.3  | 3022   | 9  | US-11-218-305-9897    | Sequence 9897, Ap |
|        | 24  | 539    | 13.1  | 2891   | 8  | US-11-266-748A-25857  | Sequence 25857, A |
|        | 25  | 530.5  | 12.9  | 3827   | 6  | US-10-449-902-18529   | Sequence 18529, A |
|        | 26  | 528.5  | 12.9  | 2729   | 6  | US-10-449-902-14548   | Sequence 14548, A |
|        | 27  | 511.5  | 12.4  | 2115   | 8  | US-11-217-529-698     | Sequence 698, App |
|        | 28  | 500    | 12.2  | 2115   | 8  | US-11-217-529-76256   | Sequence 76256, A |
|        | 29  | 450    | 10.9  | 3290   | 6  | US-10-449-902-16439   | Sequence 16439, A |
|        | 30  | 442    | 10.7  | 1641   | 6  | US-10-539-723-4       | Sequence 4, Appli |
|        | 31  | 404    | 9.8   | 15294  | 6  | US-10-547-660-15      | Sequence 15, Appl |
|        | 32  | 330.5  | 8.0   | 640    | 8  | US-11-266-748A-119619 | Sequence 119619,  |
| c      | 33  | 330.5  | 8.0   | 641    | 8  | US-11-266-748A-81241  | Sequence 81241, A |
|        | 34  | 330.5  | 8.0   | 641    | 8  | US-11-266-748A-134052 | Sequence 134052,  |
|        | 35  | 320.5  | 7.8   | 1118   | 8  | US-11-266-748A-228183 | Sequence 228183,  |
|        | 36  | 247    | 6.0   | 1338   | 9  | US-11-316-535A-21     | Sequence 21, Appl |
|        | 37  | 239    | 5.8   | 1974   | 9  | US-11-275-569-15      | Sequence 15, Appl |
|        | 38  | 231.5  | 5.6   | 4079   | 9  | US-11-218-305-206     | Sequence 206, App |
|        | 39  | 216    | 5.3   | 2301   | 9  | US-11-348-413-6910    | Sequence 6910, Ap |
|        | 40  | 213    | 5.2   | 1323   | 9  | US-11-316-535A-39     | Sequence 39, Appl |
|        | 41  | 209    | 5.1   | 1749   | 9  | US-11-316-535A-178    | Sequence 178, App |
|        | 42  | 201    | 4.9   | 1353   | 9  | US-11-316-535A-122    | Sequence 122, App |
|        | 43  | 199    | 4.8   | 1704   | 9  | US-11-348-413-4882    | Sequence 4882, Ap |
|        | 44  | 198.5  | 4.8   | 1202   | 8  | US-11-266-748A-8695   | Sequence 8695, Ap |



45 197.5 4.8 3525 9 US-11-348-413-2401

Sequence 2401, Ap

## ALIGNMENTS

## RESULT 1

US-11-330-822-38

; Sequence 38, Application US/11330822

; Publication No. US20060150281A1

; GENERAL INFORMATION:

; APPLICANT: GUAN, HANPING

; APPLICANT: KEELING, PETER L.

; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN

; TITLE OF INVENTION: HOSTS

; FILE REFERENCE: 15053-04

; CURRENT APPLICATION NUMBER: US/11/330,822

; CURRENT FILING DATE: 2006-01-11

; PRIOR APPLICATION NUMBER: PCT/US98/06660

; PRIOR FILING DATE: 1998-04-03

; PRIOR APPLICATION NUMBER: 60/042,939

; PRIOR FILING DATE: 1997-04-04

; NUMBER OF SEQ ID NOS: 86

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 38

; LENGTH: 2361

; TYPE: DNA

; ORGANISM: Escherichia coli

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(2184)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (2188)..(2280)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (2284)..(2361)

US-11-330-822-38

## Alignment Scores:

|                        |           |               |      |
|------------------------|-----------|---------------|------|
| Pred. No.:             | 9.77e-233 | Length:       | 2361 |
| Score:                 | 2462.50   | Matches:      | 451  |
| Percent Similarity:    | 74.2%     | Conservative: | 103  |
| Best Local Similarity: | 60.4%     | Mismatches:   | 174  |
| Query Match:           | 59.9%     | Indels:       | 19   |
| DB:                    | 9         | Gaps:         | 6    |

US-10-705-195-2 (1-762) x US-11-330-822-38 (1-2361)

|    |     |  |     |
|----|-----|--|-----|
| Qy | 17  | GluArgGlnIleIleAspSerLeuPheAlaAlaThrHisSerAspProPheAlaTyrLeu | 36  |
| Db | 16  | GATAGAGACGTGATTAACGCGCTAATGCAGGCCATTTTGCAGGATCCTTTTCCGTACTG  | 75  |
| Qy | 37  | GlyArgHisArgValAsnAspGluArgGluAlaValArgValLeuArgProAspAlaHis | 56  |
| Db | 76  | GGAATGCATAAAACCACCGCGGGACTGGAA---GTCCGTGCCCTTTTACCCGACGCTACC | 132 |
| Qy | 57  | HisIleAspIleIleAspArgHisThrGlyAlaValIleMetProSerGluLysIleAsp | 76  |
| Db | 133 | GATGTGTGGGTGATTGAACCGAAACCGGGCGCAAACTCGCAAACTGGAGTGTCTCGAC   | 192 |
| Qy | 77  | GluArgGlyLeuPheAlaAlaValLeuProGluHisAlaPro-----AspTyrAlaLeu  | 94  |

|    |      |   |      |
|----|------|---|------|
| Db | 193  | TCACGGGGATTCTTTAGCGGCGTCATTCCGCGACGTAAGAATTTTTTCCGCTATCAGTTG  | 252  |
| Qy | 95   | LeuValThrTyrHisGluGlyGluAlaAlaValArgGluGluAspAspTyrArgPheGly  | 114  |
| Db | 253  | GCTGTTGTCTGGCATGGTCAGCAAAACCTGATT-----GATGATCCTTACCGTTTGGT    | 306  |
| Qy | 115  | SerAlaLeuGlnHisThrAspAlaTrpLeuLeuGlyGluGlyThrHisLeuArgProTyr  | 134  |
| Db | 307  | CCGCTAATCCAGGAAATGGATGCCTGGCTATTATCTGAAGGTACTCACCTGCGCCCGTAT  | 366  |
| Qy | 135  | GluThrLeuGlyAlaHisPheAlaGluMetAspGlyValSerGlyValArgPheAlaVal  | 154  |
| Db | 367  | GAAACCTTAGGCGCGCATGCAGATACTATGGATGGCGTCACAGGTACGCGTTTCTCTGTC  | 426  |
| Qy | 155  | TrpAlaProAsnAlaArgArgValSerValIleGlyGluPheAsnGlyTrpAspSerArg  | 174  |
| Db | 427  | TGGGCTCCAAACGCCCGTCGGGTCTCGGTGGTTGGGCAATTCAACTACTGGGACGGTCGC  | 486  |
| Qy | 175  | ArgHisAlaMetArgProHisThrGlyAsnGlyLeuTrpAspIlePheIleProGlyVal  | 194  |
| Db | 487  | CGTCACCCGATGCGCCTGCGTAAAGAGAGCGGCATCTGGGAAGTGTATCCCTGGGGCG    | 546  |
| Qy | 195  | GlyLeuAsnAlaLeuTyrLysPheSerValLeuAspAlaAsnGlyAsnIleArgGluLys  | 214  |
| Db | 547  | CATAACGGTCAGCTCTATAAATACGAGATGATTGATGCCAATGGCAACTTGCCTCTGAAG  | 606  |
| Qy | 215  | AlaAspProTyrAlaPheGlyAlaGluLeuArgProThrThrAlaSerValValArgGly  | 234  |
| Db | 607  | TCCGACCCTTATGCCTTTGAAGCGCAAATGCGCCCGAAACCGCGTCTCTTATTTGCGGG   | 666  |
| Qy | 235  | LeuProAlaLysAlaGluAlaProAlaPheArgArgArgAlaAsnSerValGluAlaPro  | 254  |
| Db | 667  | CTGCCGGAAGGTTGTACAGACTGAAGAGCGCAAAAAGCGAATCAGTTTGATGCGCCA     | 726  |
| Qy | 255  | IleSerIleTyrGluValHisLeuGlySerTrpArgArgAsnProGluAsnAsnTyrTrp  | 274  |
| Db | 727  | ATCTCTATTTATGAAGTTCACCTGGGTTCCTGGCGTCGCCACACCGACAACAATTTCTGG  | 786  |
| Qy | 275  | LeuThrTyrThrGlnLeuAlaAspGluLeuValAsnTyrValLysAspMetGlyPheThr  | 294  |
| Db | 787  | TTGAGCTACCGCGAGCTGGCCGATCAACTGGTGCCTTATGCTAAATGGATGGGCTTTACC  | 846  |
| Qy | 295  | HisIleGluLeuLeuProLeuSerGluTyrProPheAspGlySerTrpGlyTyrGlnAla  | 314  |
| Db | 847  | CACCTCGAACTACTGCCCATTAAACGAGCATCCCTTCGATGGCAGTTGGGGTTATCAGCCA | 906  |
| Qy | 315  | ThrGlyLeuTyrAlaProThrSerArgPheGlySerProAspGluLeuLysAlaLeuIle  | 334  |
| Db | 907  | ACCGGCCTGTATGCGCCAACCCGCCGTTTTGGTACTCGCGACGACTTCCGTTATTTTCATT | 966  |
| Qy | 335  | AspAlaAlaHisAlaAlaGlyIleSerValIleLeuAspTrpValAlaGlyHisPhePro  | 354  |
| Db | 967  | GATGCCGACACGCAGCTGGTCTGAACGTGATTCTCGACTGGGTGCCAGGCCACTTCCCG   | 1026 |
| Qy | 355  | ThrAspAspHisGlyLeuAsnThrPheAspGlyThrAlaLeuTyrGluHisAlaAspPro  | 374  |
| Db | 1027 | ACTGATGACTTTGCGCTTGCCGAATTTGATGGCACGAACCTGTATGAACACAGCGATCCG  | 1086 |
| Qy | 375  | ArgGluGlyTyrHisGlnAspTrpAsnThrLeuIleTyrAsnPheGlyArgAsnGluVal  | 394  |

## SCORE Search Results Details for Application 10705195 and Search Result us-10-705-195-2.p2n.rnpbn

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10705195 and Search Result us-10-705-195-2.p2n.rnpbn.

[start](#)

[Go Back to Application List](#)

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 22, 2006, 19:56:13 ; Search time 495 Seconds  
(without alignments)  
3691.235 Million cell updates/sec

Title: US-10-705-195-2  
Perfect score: 4112  
Sequence: 1 MNRNRHIRRGYHPEAGERQI.....QTALRADKQPAVKDKQAKAK 762

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+\_p2n.model -DEV=xlh  
-Q=/abss/ABSSWEB\_spool/US10705195/runat\_22082006\_095558\_1059/app\_query.fasta\_1  
-DB=Published\_Applications\_NA\_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abss04  
-USER=US10705195\_CGN\_1\_1\_209\_@runat\_22082006\_095558\_1059 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_NA\_New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*

4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq1:\*  
 9: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq2:\*  
 10: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Query  |              | DB ID |    |                       |  | Description       |
|------------|--------|--------------|-------|----|-----------------------|--|-------------------|
|            | Score  | Match Length | DB    | ID |                       |  |                   |
| 1          | 2462.5 | 59.9         | 2361  | 9  | US-11-330-822-38      |  | Sequence 38, Appl |
| 2          | 2462   | 59.9         | 2187  | 9  | US-11-275-569-17      |  | Sequence 17, Appl |
| 3          | 1224.5 | 29.8         | 1869  | 9  | US-11-348-413-6911    |  | Sequence 6911, Ap |
| 4          | 618.5  | 15.0         | 2668  | 9  | US-11-056-355B-76595  |  | Sequence 76595, A |
| 5          | 614.5  | 14.9         | 2763  | 9  | US-11-056-355B-99154  |  | Sequence 99154, A |
| 6          | 614.5  | 14.9         | 2763  | 9  | US-11-056-355B-110393 |  | Sequence 110393,  |
| 7          | 614.5  | 14.9         | 2764  | 6  | US-10-953-349-4536    |  | Sequence 4536, Ap |
| 8          | 614.5  | 14.9         | 2764  | 9  | US-11-056-355B-27071  |  | Sequence 27071, A |
| 9          | 614.5  | 14.9         | 2764  | 9  | US-11-056-355B-30239  |  | Sequence 30239, A |
| 10         | 614.5  | 14.9         | 2764  | 9  | US-11-056-355B-33829  |  | Sequence 33829, A |
| 11         | 604.5  | 14.7         | 3643  | 8  | US-11-216-545-3261    |  | Sequence 3261, Ap |
| 12         | 598    | 14.5         | 2588  | 9  | US-11-056-355B-100250 |  | Sequence 100250,  |
| 13         | 598    | 14.5         | 2588  | 9  | US-11-056-355B-111489 |  | Sequence 111489,  |
| 14         | 593    | 14.4         | 2759  | 9  | US-11-218-305-12548   |  | Sequence 12548, A |
| 15         | 592.5  | 14.4         | 2763  | 9  | US-11-056-355B-19641  |  | Sequence 19641, A |
| 16         | 592.5  | 14.4         | 2763  | 9  | US-11-056-355B-19806  |  | Sequence 19806, A |
| 17         | 592.5  | 14.4         | 2826  | 9  | US-11-218-305-12549   |  | Sequence 12549, A |
| 18         | 587    | 14.3         | 2640  | 9  | US-11-330-822-58      |  | Sequence 58, Appl |
| 19         | 569    | 13.8         | 3553  | 6  | US-10-449-902-12839   |  | Sequence 12839, A |
| 20         | 566    | 13.8         | 2649  | 6  | US-10-539-723-6       |  | Sequence 6, Appli |
| 21         | 547.5  | 13.3         | 2763  | 9  | US-11-330-822-60      |  | Sequence 60, Appl |
| 22         | 547.5  | 13.3         | 2790  | 9  | US-11-056-355B-11438  |  | Sequence 11438, A |
| 23         | 547.5  | 13.3         | 3022  | 9  | US-11-218-305-9897    |  | Sequence 9897, Ap |
| 24         | 539    | 13.1         | 2891  | 8  | US-11-266-748A-25857  |  | Sequence 25857, A |
| 25         | 530.5  | 12.9         | 3827  | 6  | US-10-449-902-18529   |  | Sequence 18529, A |
| 26         | 528.5  | 12.9         | 2729  | 6  | US-10-449-902-14548   |  | Sequence 14548, A |
| 27         | 511.5  | 12.4         | 2115  | 8  | US-11-217-529-698     |  | Sequence 698, App |
| 28         | 500    | 12.2         | 2115  | 8  | US-11-217-529-76256   |  | Sequence 76256, A |
| 29         | 450    | 10.9         | 3290  | 6  | US-10-449-902-16439   |  | Sequence 16439, A |
| 30         | 442    | 10.7         | 1641  | 6  | US-10-539-723-4       |  | Sequence 4, Appli |
| 31         | 404    | 9.8          | 15294 | 6  | US-10-547-660-15      |  | Sequence 15, Appl |
| 32         | 330.5  | 8.0          | 640   | 8  | US-11-266-748A-119619 |  | Sequence 119619,  |
| c 33       | 330.5  | 8.0          | 641   | 8  | US-11-266-748A-81241  |  | Sequence 81241, A |
| 34         | 330.5  | 8.0          | 641   | 8  | US-11-266-748A-134052 |  | Sequence 134052,  |
| 35         | 320.5  | 7.8          | 1118  | 8  | US-11-266-748A-228183 |  | Sequence 228183,  |
| 36         | 247    | 6.0          | 1338  | 9  | US-11-316-535A-21     |  | Sequence 21, Appl |
| 37         | 239    | 5.8          | 1974  | 9  | US-11-275-569-15      |  | Sequence 15, Appl |
| 38         | 231.5  | 5.6          | 4079  | 9  | US-11-218-305-206     |  | Sequence 206, App |
| 39         | 216    | 5.3          | 2301  | 9  | US-11-348-413-6910    |  | Sequence 6910, Ap |
| 40         | 213    | 5.2          | 1323  | 9  | US-11-316-535A-39     |  | Sequence 39, Appl |
| 41         | 209    | 5.1          | 1749  | 9  | US-11-316-535A-178    |  | Sequence 178, App |
| 42         | 201    | 4.9          | 1353  | 9  | US-11-316-535A-122    |  | Sequence 122, App |
| 43         | 199    | 4.8          | 1704  | 9  | US-11-348-413-4882    |  | Sequence 4882, Ap |
| 44         | 198.5  | 4.8          | 1202  | 8  | US-11-266-748A-8695   |  | Sequence 8695, Ap |

45 197.5 4.8 3525 9 US-11-348-413-2401

Sequence 2401, Ap

## ALIGNMENTS

## RESULT 1

US-11-330-822-38

; Sequence 38, Application US/11330822

; Publication No. US20060150281A1

; GENERAL INFORMATION:

; APPLICANT: GUAN, HANPING

; APPLICANT: KEELING, PETER L.

; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN

; TITLE OF INVENTION: HOSTS

; FILE REFERENCE: 15053-04

; CURRENT APPLICATION NUMBER: US/11/330,822

; CURRENT FILING DATE: 2006-01-11

; PRIOR APPLICATION NUMBER: PCT/US98/06660

; PRIOR FILING DATE: 1998-04-03

; PRIOR APPLICATION NUMBER: 60/042,939

; PRIOR FILING DATE: 1997-04-04

; NUMBER OF SEQ ID NOS: 86

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 38

; LENGTH: 2361

; TYPE: DNA

; ORGANISM: Escherichia coli

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(2184)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (2188)..(2280)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (2284)..(2361)

US-11-330-822-38

## Alignment Scores:

|                        |           |               |      |
|------------------------|-----------|---------------|------|
| Pred. No.:             | 9.77e-233 | Length:       | 2361 |
| Score:                 | 2462.50   | Matches:      | 451  |
| Percent Similarity:    | 74.2%     | Conservative: | 103  |
| Best Local Similarity: | 60.4%     | Mismatches:   | 174  |
| Query Match:           | 59.9%     | Indels:       | 19   |
| DB:                    | 9         | Gaps:         | 6    |

US-10-705-195-2 (1-762) x US-11-330-822-38 (1-2361)

|    |     |   |     |
|----|-----|---|-----|
| Qy | 17  | GluArgGlnIleIleAspSerLeuPheAlaAlaThrHisSerAspProPheAlaTyrLeu    | 36  |
| Db | 16  | GATAGAGACGTGATTAACGCGCTAATTGCAGGCCATTTTGC GGATCCTTTTCCG TACTG   | 75  |
| Qy | 37  | GlyArgHisArgValAsnAspGluArgGluAlaValArgValLeuArgProAspAlaHis    | 56  |
| Db | 76  | GGAATGCATAAAACCACCGCGG GACTGGAA---GTCCGTGCCCTTTTACCCGACGCTACC   | 132 |
| Qy | 57  | HisIleAspIleIleAspArgHisThrGlyAlaValIleMetProSerGluLysIleAsp    | 76  |
| Db | 133 | GATGTGTGGGTGATTGAACCGAAAACCGGGCGCAA AACTCGCAA AACTGGAGTGTCTCGAC | 192 |
| Qy | 77  | GluArgGlyLeuPheAlaAlaValLeuProGluHisAlaPro-----AspTyrAlaLeu     | 94  |

|    |      |   |      |
|----|------|---|------|
| Db | 193  | TCACGGGGATTCTTTAGCGGCGTCATTCCGCGACGTAAGAATTTTTTCCGCTATCAGTTG  | 252  |
| Qy | 95   | LeuValThrTyrHisGluGlyGluAlaAlaValArgGluGluAspAspTyrArgPheGly  | 114  |
| Db | 253  | GCTGTTGTCTGGCATGGTCAGCAAACCTGATT-----GATGATCCTTACCGTTTGGT     | 306  |
| Qy | 115  | SerAlaLeuGlnHisThrAspAlaTrpLeuLeuGlyGluGlyThrHisLeuArgProTyr  | 134  |
| Db | 307  | CCGCTAATCCAGGAAATGGATGCCTGGCTATTATCTGAAGGTACTCACCTGCGCCCGTAT  | 366  |
| Qy | 135  | GluThrLeuGlyAlaHisPheAlaGluMetAspGlyValSerGlyValArgPheAlaVal  | 154  |
| Db | 367  | GAAACCTTAGGCGCGCATGCAGATACTATGGATGGCGTCACAGGTACGCGTTTCTCTGTC  | 426  |
| Qy | 155  | TrpAlaProAsnAlaArgArgValSerValIleGlyGluPheAsnGlyTrpAspSerArg  | 174  |
| Db | 427  | TGGGCTCCAAACGCCCGTCGGGTCTCGGTGGTTGGGCAATTCAACTACTGGGACGGTCGC  | 486  |
| Qy | 175  | ArgHisAlaMetArgProHisThrGlyAsnGlyLeuTrpAspIlePheIleProGlyVal  | 194  |
| Db | 487  | CGTCACCCGATGCGCCTGCGTAAAGAGAGCGGCATCTGGGAACGTGTTTATCCCTGGGGCG | 546  |
| Qy | 195  | GlyLeuAsnAlaLeuTyrLysPheSerValLeuAspAlaAsnGlyAsnIleArgGluLys  | 214  |
| Db | 547  | CATAACGGTCAGCTCTATAAATACGAGATGATTGATGCCAATGGCAACTTGCCTCTGAAG  | 606  |
| Qy | 215  | AlaAspProTyrAlaPheGlyAlaGluLeuArgProThrThrAlaSerValValArgGly  | 234  |
| Db | 607  | TCCGACCCTTATGCCTTTGAAGCGCAAATGCGCCCGAAACCGCGTCTCTTATTTGCGGG   | 666  |
| Qy | 235  | LeuProAlaLysAlaGluAlaProAlaPheArgArgAlaAsnSerValGluAlaPro     | 254  |
| Db | 667  | CTGCCGGAAGGTTGTACAGACTGAAGAGCGCAAAAAGCGAATCAGTTTGATGCGCCA     | 726  |
| Qy | 255  | IleSerIleTyrGluValHisLeuGlySerTrpArgArgAsnProGluAsnAsnTyrTrp  | 274  |
| Db | 727  | ATCTCTATTTATGAAGTTCACCTGGGTCTCTGGCGTCGCCACACCGACAACAATTTCTGG  | 786  |
| Qy | 275  | LeuThrTyrThrGlnLeuAlaAspGluLeuValAsnTyrValLysAspMetGlyPheThr  | 294  |
| Db | 787  | TTGAGCTACCGCGAGCTGGCCGATCAACTGGTGCCTTATGCTAAATGGATGGGCTTTACC  | 846  |
| Qy | 295  | HisIleGluLeuLeuProLeuSerGluTyrProPheAspGlySerTrpGlyTyrGlnAla  | 314  |
| Db | 847  | CACCTCGAACTACTGCCCATTAAACGAGCATCCCTTCGATGGCAGTTGGGGTTATCAGCCA | 906  |
| Qy | 315  | ThrGlyLeuTyrAlaProThrSerArgPheGlySerProAspGluLeuLysAlaLeuIle  | 334  |
| Db | 907  | ACCGGCCTGTATGCGCCAACCCGCCGTTTGGTACTCGCGACGACTTCCGTTATTTTCATT  | 966  |
| Qy | 335  | AspAlaAlaHisAlaAlaGlyIleSerValIleLeuAspTrpValAlaGlyHisPhePro  | 354  |
| Db | 967  | GATGCCGCACACGAGCTGGTCTGAACGTGATTCTCGACTGGGTGCCAGGCCACTTCCCG   | 1026 |
| Qy | 355  | ThrAspAspHisGlyLeuAsnThrPheAspGlyThrAlaLeuTyrGluHisAlaAspPro  | 374  |
| Db | 1027 | ACTGATGACTTTGCGCTTGCCGAATTTGATGGCACGAACTTGATGAACACAGCGATCCG   | 1086 |
| Qy | 375  | ArgGluGlyTyrHisGlnAspTrpAsnThrLeuIleTyrAsnPheGlyArgAsnGluVal  | 394  |

Comments /  
Suggestions

2: gb\_est3:\*  
 3: gb\_est4:\*  
 4: gb\_est5:\*  
 5: gb\_est6:\*  
 6: gb\_htc:\*  
 7: gb\_est2:\*  
 8: gb\_est7:\*  
 9: gb\_est8:\*  
 10: gb\_est9:\*  
 11: gb\_gss1:\*  
 12: gb\_gss2:\*  
 13: gb\_gss3:\*  
 14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|        |       | %      |        |      |    |          | Description        |
|--------|-------|--------|--------|------|----|----------|--------------------|
| Result | Query | Match  | Length | DB   | ID |          |                    |
| No.    | Score |        |        |      |    |          |                    |
| c      | 1     | 1159.5 | 28.2   | 1261 | 12 | CG755636 | CG755636 P051-1-G0 |
| c      | 2     | 1075   | 26.1   | 1342 | 12 | CG755637 | CG755637 P051-1-G0 |
|        | 3     | 947.5  | 23.0   | 1003 | 14 | DU773085 | DU773085 APKG3284. |
|        | 4     | 919    | 22.3   | 922  | 14 | DU787945 | DU787945 APKH2378. |
| c      | 5     | 881.5  | 21.4   | 1008 | 14 | DU785952 | DU785952 APKH1378. |
|        | 6     | 756    | 18.4   | 1035 | 14 | DU743159 | DU743159 ASNC1588. |
| c      | 7     | 738.5  | 18.0   | 1161 | 12 | CG752267 | CG752267 P046-4-G1 |
|        | 8     | 729.5  | 17.7   | 1163 | 12 | BZ569819 | BZ569819 msh2_1033 |
|        | 9     | 715    | 17.4   | 634  | 13 | CL675608 | CL675608 PRI0115b_ |
|        | 10    | 669    | 16.3   | 528  | 13 | CL667597 | CL667597 PRI0155c_ |
|        | 11    | 661    | 16.1   | 732  | 12 | CG410928 | CG410928 RM1062 Lx |
|        | 12    | 656    | 16.0   | 584  | 1  | AJ879817 | AJ879817 AJ879817  |
|        | 13    | 652    | 15.9   | 1060 | 11 | BZ557122 | BZ557122 pacs1-60_ |
| c      | 14    | 623    | 15.2   | 543  | 11 | BH783525 | BH783525 fzmb013f0 |
| c      | 15    | 613    | 14.9   | 755  | 12 | CG410929 | CG410929 RM1063 Lx |
|        | 16    | 581.5  | 14.1   | 3039 | 13 | CL968925 | CL968925 OsIFCC017 |
| c      | 17    | 579.5  | 14.1   | 605  | 12 | CG411045 | CG411045 RM359 Lxx |
|        | 18    | 555    | 13.5   | 2478 | 13 | CL966805 | CL966805 OsIFCC014 |
|        | 19    | 553    | 13.4   | 2766 | 6  | AY109521 | AY109521 Zea mays  |
|        | 20    | 550    | 13.4   | 417  | 14 | DX059445 | DX059445 KBrB065F1 |
|        | 21    | 547    | 13.3   | 2738 | 6  | AK009815 | AK009815 Mus muscu |
|        | 22    | 547    | 13.3   | 2862 | 6  | AK050365 | AK050365 Mus muscu |
|        | 23    | 535.5  | 13.0   | 3012 | 6  | AY105679 | AY105679 Zea mays  |
|        | 24    | 532    | 12.9   | 443  | 5  | CK339918 | CK339918 C0871G07- |
|        | 25    | 514.5  | 12.5   | 3305 | 6  | AK050423 | AK050423 Mus muscu |
|        | 26    | 504    | 12.3   | 2732 | 6  | AY109532 | AY109532 Zea mays  |
|        | 27    | 495    | 12.0   | 2044 | 14 | AY413117 | AY413117 Mus muscu |
| c      | 28    | 493    | 12.0   | 1569 | 12 | CG755635 | CG755635 P051-1-G0 |
|        | 29    | 492.5  | 12.0   | 717  | 1  | AJ797306 | AJ797306 AJ797306  |
|        | 30    | 474    | 11.5   | 2109 | 14 | AY413115 | AY413115 Homo sapi |
|        | 31    | 474    | 11.5   | 2109 | 14 | AY413116 | AY413116 Pan trogl |
|        | 32    | 470.5  | 11.4   | 1275 | 6  | AY811197 | AY811197 Schistoso |
| c      | 33    | 470.5  | 11.4   | 1482 | 11 | BH770747 | BH770747 LLMGtag49 |
|        | 34    | 451    | 11.0   | 504  | 12 | CG411053 | CG411053 RM367 Lxx |
| c      | 35    | 442.5  | 10.8   | 609  | 12 | CG411057 | CG411057 RM372 Lxx |
| c      | 36    | 429.5  | 10.4   | 439  | 12 | CG411069 | CG411069 RM384 Lxx |
| c      | 37    | 418    | 10.2   | 1317 | 12 | BZ572034 | BZ572034 msh2_240. |
|        | 38    | 417.5  | 10.2   | 852  | 5  | CD438018 | CD438018 EL01N0508 |



|    |       |     |      |    |          |                    |
|----|-------|-----|------|----|----------|--------------------|
| 39 | 401   | 9.8 | 316  | 5  | CK339021 | CK339021 C0821D11- |
| 40 | 396.5 | 9.6 | 1167 | 5  | CD664476 | CD664476 TVEST020. |
| 41 | 393.5 | 9.6 | 825  | 8  | CO467539 | CO467539 MZCCL2004 |
| 42 | 388.5 | 9.4 | 843  | 8  | CO098553 | CO098553 GR_Ea22P  |
| 43 | 379.5 | 9.2 | 906  | 8  | CO456486 | CO456486 MZCCL2000 |
| 44 | 377   | 9.2 | 1411 | 10 | DT989097 | DT989097 CLJ241-E0 |
| 45 | 375   | 9.1 | 706  | 5  | CF638461 | CF638461 D02_H06 F |

## ALIGNMENTS

## RESULT 1

CG755636/c

LOCUS CG755636 1261 bp DNA linear GSS 24-OCT-2003

DEFINITION P051-1-G03.yb Ppa EcoRI BAC Library *Pristionchus pacificus* genomic, genomic survey sequence.

ACCESSION CG755636

VERSION CG755636.1 GI:37982332

KEYWORDS GSS.

SOURCE *Pristionchus pacificus*ORGANISM *Pristionchus pacificus*Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; *Pristionchus*.

REFERENCE 1 (bases 1 to 1261)

AUTHORS Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,  
Buntjer,J., van der Meulen,M. and Sommer,R.J.TITLE An integrated physical and genetic map of the nematode *Pristionchus pacificus*

JOURNAL Mol. Genet. Genomics 269 (5), 715-722 (2003)

PUBMED 12884007

COMMENT Contact: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

Class: BAC ends.

FEATURES Location/Qualifiers

source 1. .1261

/organism="*Pristionchus pacificus*"

/mol\_type="genomic DNA"

/strain="California"

/db\_xref="taxon:54126"

/clone\_lib="Ppa EcoRI BAC Library"

/note="The library was generated by a partial digest of  
the genomic DNA with EcoRI and cloning into the BAC  
vector."

## ORIGIN

## Alignment Scores:

|                        |           |               |      |
|------------------------|-----------|---------------|------|
| Pred. No.:             | 3.18e-115 | Length:       | 1261 |
| Score:                 | 1159.50   | Matches:      | 218  |
| Percent Similarity:    | 79.6%     | Conservative: | 40   |
| Best Local Similarity: | 67.3%     | Mismatches:   | 60   |
| Query Match:           | 28.2%     | Indels:       | 6    |
| DB:                    | 12        | Gaps:         | 2    |

US-10-705-195-2 (1-762) x CG755636 (1-1261)

Qy 133 ProTyrGluThrLeuGlyAlaHisPheAlaGlu-----MetAspGlyValSerGlyVal 150

|    |      |  |  |     |    |  |     |
|----|------|--|--|-----|----|--|-----|
| Db | 1050 |  |  |     |    | CCGTATGAAACCTTTAGGCGGCGCCATGCAGGATACCTATGGATGGGGGTCACCAGGTA  | 991 |
| Qy | 151  | Arg---   | PheAlaVal-TrpAlaProAsnAlaArg-ArgValSerValIleGlyGluPheA | 169 |    |  |     |
| Db | 990  |  | ::   |     |    | CGCGTTTTCTCTGTTTTGGGCTCCAAACGCCCGTTCGGGTCTCGGTGGTGGGCAATTCA  | 931 |
| Qy | 169  | snGlyTrpAspSerArgArgHisAlaMetArgProHisThrGlyAsnGlyLeuTrpAspI | 189  |     |    |  |     |
| Db | 930  |  |  |     |    | ACTACTGGGACGGTCGCCGTCACCCGATGCCCTGCGTAAAGAGAGCGGCATCTGGGAAC  | 871 |
| Qy | 189  | lePheIleProGlyValGlyLeuAsnAlaLeu-TyrLysPheSerValLeuAspAlaAsn | 208  |     |    |  |     |
| Db | 870  | ::   |  |     |    | TGTTTATCCCTGGGGCGCATAACGGTCAGCTCTTATAAATACGAGATGATTGATGCCAAT | 811 |
| Qy | 209  | GlyAsnIleArgGluLysAlaAspProTyrAlaPheGlyAlaGluLeuArgProThrThr | 228  |     |    |  |     |
| Db | 810  |  | ::   |     |    | GGCAACTTGCGTCTGAAGTCCGACCTTATGCCTTCGAAGCGCAAATGCGCCCGAAACC   | 751 |
| Qy | 229  | AlaSerValValArgGlyLeuProAlaLysAlaGluAlaProAlaPheArgArgArgAla | 248  |     |    |  |     |
| Db | 750  |  | ::   |     |    | GCGTCTCTTATTTGCGGGCTGCCGAAAAGGTTGTACAGACTGAAGAGCGCAAAAAGCG   | 691 |
| Qy | 249  | AsnSerValGluAlaProIleSerIleTyrGluValHisLeuGlySerTrpArgArgAsn | 268  |     |    |  |     |
| Db | 690  |  | ::   |     |    | AATCAGTTTGATGCGCCAATCTCTATTTATGAAGTTCACCTGGGTTCCTGGCGTCGCCAC | 631 |
| Qy | 269  | ProGluAsnAsnTyrTrpLeuThrTyrThrGlnLeuAlaAspGluLeuValAsnTyrVal | 288  |     |    |  |     |
| Db | 630  | ::   |  | ::  |    | ACCGACAACAATTTCTGGTTGAGCTACCGCGAGCTGGCCGATCAACTGGTGCCTTATGCT | 571 |
| Qy | 289  | LysAspMetGlyPheThrHisIleGluLeuLeuProLeuSerGluTyrProPheAspGly | 308  |     |    |  |     |
| Db | 570  |  |  | ::  |    | AAATGGATGGGCTTTACCCACCTCGAACTACTGCCCATTAACGAGCATCCCTTCGATGGC | 511 |
| Qy | 309  | SerTrpGlyTyrGlnAlaThrGlyLeuTyrAlaProThrSerArgPheGlySerProAsp | 328  |     |    |  |     |
| Db | 510  |  |  |     | :: | AGTTGGGGTTATCAGCCAACCGGCCTGTATGCACCAACCGCCGTTTTGGTACTCGCGAC  | 451 |
| Qy | 329  | GluLeuLysAlaLeuIleAspAlaAlaHisAlaAlaGlyIleSerValIleLeuAspTrp | 348  |     |    |  |     |
| Db | 450  | ::   | ::   |     |    | GACTTCCGTTATTTTATTGATGCCGCACACGCAGCTGGTCTGAACGTGATTCTCGACTGG | 391 |
| Qy | 349  | ValAlaGlyHisPheProThrAspAspHisGlyLeuAsnThrPheAspGlyThrAlaLeu | 368  |     |    |  |     |
| Db | 390  |  |  |     |    | GTGCCAGGCCACTTCCCGACCGATGACTTTGCGCTTGCCGAATTTGATGGCACGAACCTG | 331 |
| Qy | 369  | TyrGluHisAlaAspProArgGluGlyTyrHisGlnAspTrpAsnThrLeuIleTyrAsn | 388  |     |    |  |     |
| Db | 330  |  | ::   |     |    | TATGAACACAGCGATCCGCGTGAAGGCTATCATCAGGACTGGAACACGCTGATCTACAAC | 271 |
| Qy | 389  | PheGlyArgAsnGluValLysAsnPheLeuGlnGlyAsnAlaLeuTyrTrpIleGluArg | 408  |     |    |  |     |
| Db | 270  | ::   |  |     |    | TATGGTCGCCGTGAAGTCAGTAACTTCCTCGTCGGTAACGCGCTTTACTGGATTGAACGT | 211 |
| Qy | 409  | PheGlyPheAspGlyIleArgValAspAlaValAlaSerMetIleTyrArgAsnTyrSer | 428  |     |    |  |     |
| Db | 210  |  |  | ::  |    | TTTGGTATTGATGCGCTGCGCGTCGATGCGGTGCGGTCAATGATTTATCGCGACTACAGC | 151 |
| Qy | 429  | ArgLysAspGlyGluTrpIleProAsnArgTyrGlyGlySerGluAsnLeuGluAlaIle | 448  |     |    |  |     |
|    |      |  | ::   |     |    |  |     |

# SCORE Search Results Details for Application 10705195 and Search Result us-10-705-195-1.rst.

[Score Home Page](#)
[Retrieve Application List](#)
[SCORE System Overview](#)
[SCORE FAQ](#)
[Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10705195 and Search Result us-10-705-195-1.rst.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 22, 2006, 19:25:16 ; Search time 10532 Seconds  
(without alignments)  
13140.937 Million cell updates/sec

Title: US-10-705-195-1  
Perfect score: 2475  
Sequence: 1 actgtatgccgtgcagctgg.....taaagcggcaccatactgcc 2475

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_htc:\*  
7: gb\_est2:\*  
8: gb\_est7:\*  
9: gb\_est8:\*  
10: gb\_est9:\*  
11: gb\_gss1:\*  
12: gb\_gss2:\*  
13: gb\_gss3:\*  
14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result | No. | Score | %     |              | DB | ID       | Description        |
|--------|-----|-------|-------|--------------|----|----------|--------------------|
|        |     |       | Query | Match Length |    |          |                    |
| c      | 1   | 421.6 | 17.0  | 1261         | 12 | CG755636 | CG755636 P051-1-G0 |
| c      | 2   | 388.4 | 15.7  | 1342         | 12 | CG755637 | CG755637 P051-1-G0 |
|        | 3   | 335.4 | 13.6  | 1003         | 14 | DU773085 | DU773085 APKG3284. |
|        | 4   | 302   | 12.2  | 922          | 14 | DU787945 | DU787945 APKH2378. |
| c      | 5   | 275.2 | 11.1  | 1161         | 12 | CG752267 | CG752267 P046-4-G1 |
|        | 6   | 262   | 10.6  | 528          | 13 | CL667597 | CL667597 PRI0155c_ |
|        | 7   | 260.8 | 10.5  | 1163         | 12 | BZ569819 | BZ569819 msh2_1033 |
|        | 8   | 258.4 | 10.4  | 634          | 13 | CL675608 | CL675608 PRI0115b_ |
| c      | 9   | 248.8 | 10.1  | 543          | 11 | BH783525 | BH783525 fzmbo13f0 |
|        | 10  | 238.6 | 9.6   | 1060         | 11 | BZ557122 | BZ557122 pacs1-60_ |
| c      | 11  | 227.2 | 9.2   | 1008         | 14 | DU785952 | DU785952 APKH1378. |
|        | 12  | 219.6 | 8.9   | 732          | 12 | CG410928 | CG410928 RM1062 Lx |
|        | 13  | 210.6 | 8.5   | 417          | 14 | DX059445 | DX059445 KBrB065F1 |
|        | 14  | 207.8 | 8.4   | 443          | 5  | CK339918 | CK339918 C0871G07- |
| c      | 15  | 203.4 | 8.2   | 605          | 12 | CG411045 | CG411045 RM359 Lxx |
|        | 16  | 203.2 | 8.2   | 584          | 1  | AJ879817 | AJ879817 AJ879817  |
|        | 17  | 195.4 | 7.9   | 971          | 14 | DU754880 | DU754880 ASNF4137. |
| c      | 18  | 194.8 | 7.9   | 755          | 12 | CG410929 | CG410929 RM1063 Lx |
| c      | 19  | 187.6 | 7.6   | 1569         | 12 | CG755635 | CG755635 P051-1-G0 |
| c      | 20  | 174.2 | 7.0   | 1317         | 12 | BZ572034 | BZ572034 msh2_240. |
| c      | 21  | 158.2 | 6.4   | 609          | 12 | CG411057 | CG411057 RM372 Lxx |
| c      | 22  | 154.8 | 6.3   | 439          | 12 | CG411069 | CG411069 RM384 Lxx |
|        | 23  | 146.8 | 5.9   | 316          | 5  | CK339021 | CK339021 C0821D11- |
|        | 24  | 146.4 | 5.9   | 504          | 12 | CG411053 | CG411053 RM367 Lxx |
|        | 25  | 144.4 | 5.8   | 671          | 2  | BI719233 | BI719233 1031042C0 |
|        | 26  | 141.4 | 5.7   | 717          | 1  | AJ797306 | AJ797306 AJ797306  |
|        | 27  | 133.6 | 5.4   | 1035         | 14 | DU743159 | DU743159 ASNC1588. |
| c      | 28  | 133   | 5.4   | 320          | 8  | CV983818 | CV983818 UMC-bof_0 |
|        | 29  | 130.8 | 5.3   | 663          | 5  | CF638951 | CF638951 D09_B01 F |
|        | 30  | 130.8 | 5.3   | 706          | 5  | CF638461 | CF638461 D02_H06 F |
|        | 31  | 113   | 4.6   | 950          | 10 | DR638327 | DR638327 EST102895 |
| c      | 32  | 112.2 | 4.5   | 361          | 13 | CZ443531 | CZ443531 contig_RS |
| c      | 33  | 109   | 4.4   | 903          | 11 | BZ554984 | BZ554984 pacs1-60_ |
| c      | 34  | 107.8 | 4.4   | 216          | 5  | CK336186 | CK336186 C0143B08- |
| c      | 35  | 106   | 4.3   | 1242         | 12 | BZ572104 | BZ572104 msh2_2516 |
|        | 36  | 105   | 4.2   | 729          | 2  | BF864125 | BF864125 963049D02 |
|        | 37  | 104.8 | 4.2   | 575          | 1  | AA203085 | AA203085 LD03583:5 |
|        | 38  | 104.6 | 4.2   | 650          | 5  | CD596575 | CD596575 RK102A4B1 |
|        | 39  | 100.4 | 4.1   | 1527         | 6  | CNS0EPGI | CR635676 Tetraodon |
| c      | 40  | 99.6  | 4.0   | 1423         | 12 | BZ572026 | BZ572026 msh2_236. |
|        | 41  | 99.4  | 4.0   | 740          | 8  | CO554971 | CO554971 AGENCOURT |
|        | 42  | 99.4  | 4.0   | 747          | 8  | CO568637 | CO568637 AGENCOURT |
|        | 43  | 99.2  | 4.0   | 993          | 14 | DU745819 | DU745819 ASNC2988. |
|        | 44  | 98    | 4.0   | 697          | 8  | CV076102 | CV076102 AGENCOURT |
|        | 45  | 97.4  | 3.9   | 634          | 2  | BI890238 | BI890238 ZF637-2-0 |

## ALIGNMENTS

RESULT 1

CG755636/c

LOCUS

CG755636

1261 bp

DNA

linear

GSS 24-OCT-2003

DEFINITION P051-1-G03.yb Ppa EcoRI BAC Library *Pristionchus pacificus* genomic, genomic survey sequence.

ACCESSION CG755636

VERSION CG755636.1 GI:37982332

KEYWORDS GSS.

SOURCE *Pristionchus pacificus*

ORGANISM *Pristionchus pacificus*  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; *Pristionchus*.

REFERENCE 1 (bases 1 to 1261)

AUTHORS Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K., Buntjer,J., van der Meulen,M. and Sommer,R.J.

TITLE An integrated physical and genetic map of the nematode *Pristionchus pacificus*

JOURNAL Mol. Genet. Genomics 269 (5), 715-722 (2003)

PUBMED 12884007

COMMENT Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
Class: BAC ends.

FEATURES Location/Qualifiers

source 1. .1261  
/organism="*Pristionchus pacificus*"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Ppa EcoRI BAC Library"  
/note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC vector."

## ORIGIN

Query Match 17.0%; Score 421.6; DB 12; Length 1261;  
Best Local Similarity 67.4%; Pred. No. 1e-95;  
Matches 623; Conservative 0; Mismatches 299; Indels 2; Gaps 2;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 630 | TTTGGGCGCCCAACGCGCG-GCGGGTATCGGTCATCGGCGAATTCAACGGCTGGGACAGC | 688 |
|    |     |  |     |
| Db | 976 | TTTGGGCTCAAACGCCCGTTCGGGTCTCGGTGGTTGGGCAATTCAACTACTGGGACGGT  | 917 |
| Qy | 689 | CGCCGCCATGCCATGCGTCCGCACACAGGCAACGGCCTGTGGGACATCTTTATCCCCGGC | 748 |
|    |     |  |     |
| Db | 916 | CGCCGTCACCCGATGCCCTGCGTAAAGAGAGCGGCATCTGGGAAGTGTATCCCTGGG    | 857 |
| Qy | 749 | GTCGGCCTCAACGCGCT-GTATAAATTCTCGTACTCGATGCCAACGGCAACATCCGCGA  | 807 |
|    |     |  |     |
| Db | 856 | GCGCATAACGGTCAGCTCTTATAAATACGAGATGATTGATGCCAATGGCAACTTGCCTCT | 797 |
| Qy | 808 | AAAAGCCGACCCCTACGCATTCGGCGCGGAGCTGCGCCCGACCACCGCATCCGTGGTGCG | 867 |
|    |     |  |     |
| Db | 796 | GAAGTCCGACCCTTATGCCTTCGAAGCGCAATGCGCCCGAAACCGCGTCTCTTATTTG   | 737 |
| Qy | 868 | CGGCTTGCCGGCCAAAGCCGAAGCGCCCGCTTCCGCCCGCGCCAACTCCGTGGAAGC    | 927 |
|    |     |  |     |
| Db | 736 | CGGGCTGCCGGAAGGTTGTACAGACTGAAGAGCGCAAAAAGCGAATCAGTTTGATGC    | 677 |
| Qy | 928 | GCCCATCAGCATTTACGAAGTCCATCTCGGCTCGTGGCGGCGCAATCCCGAAAACAATA  | 987 |

```

      ||| |||  |||| |||| || || || || |||| ||| |  ||| |||| |
Db      676 GCCAATCTCTATTTATGAAGTTCACCTGGGTTCTTGGCGTCGCCACACCGACAACAATTT 617
Qy      988 CTGGCTCACCTACACGCAGCTGGCCGACGAATTGGTGAACATATGTAAAAGACATGGGCTT 1047
      |||| | | ||||  ||||| || |||||  |||| |||  |||||
Db      616 CTGGTTGAGCTACCGCGAGCTGGCCGATCAACTGGTGCCTTATGCTAAATGGATGGGCTT 557
Qy     1048 CACCCACATCGAGCTGCTGCCCTTGTCGAATATCCGTTTCGACGGCTCATGGGGCTACCA 1107
      |||| | |||| | |||| | || |||| | |||| |||  |||| | |
Db      556 TACCCACCTCGAACTACTGCCCATTAACGAGCATCCCTTCGATGGCAGTTGGGGTTATCA 497
Qy     1108 AGCCACCGGCCTGTATGCACCGACCAGCCGCTTCGGCTCGCCCGATGAGCTGAAAGCCCT 1167
      | ||||| ||||| ||||| ||| |||| | || | ||| || |
Db      496 GCCAACCGGCCTGTATGCACCAACCGCCGTTTGGTACTCGCGACGACTTCCGTTATTT 437
Qy     1168 GATTGACGCCGCCACGCCGCCGGCATCAGCGTATTCTCGACTGGGTAGCGGGGCACTT 1227
      |||| | |||| | |||| || || | | ||||| ||||| || || ||||
Db      436 CATTGATGCCGCACACGCAGCTGGTCTGAACGTGATTCTCGACTGGGTGCCAGGCCACTT 377
Qy     1228 CCCCACCGACGACCACGGCCTCAACACCTTCGACGGCACGGCGCTTTACGAACACGCCGA 1287
      ||| |||| | || | || | || | || |||| | || |||| | ||
Db      376 CCCGACCGATGACTTTGCGCTTGCCGAATTTGATGGCACGAATTGTATGAACACAGCGA 317
Qy     1288 CCCGCGGAAGGCTACCATCAGGATTGGAACACGCTGATTTACAACCTTCGGCCGCAACGA 1347
      |||| | ||||| ||||| ||||| ||||| ||||| || || || ||
Db      316 TCCGCGTGAAGGCTATCATCAGGACTGGAACACGCTGATCTACAACATATGGTCGCCGTGA 257
Qy     1348 AGTCAAAAACCTTCTGCAGGGCAACGCGCTCTACTGGATTGAGCGTTTCGGCTTCGACGG 1407
      |||| | ||||| || ||||| ||||| ||||| |||| | || |
Db      256 AGTCAGTAACTTCTCGTCGGTAACGCGCTTACTGGATTGAACGTTTTGGTATTGATGC 197
Qy     1408 CATCCGCGTGGACGCCGTGGCCTCGATGATTTACCGCAACTACTCGCGCAAAGACGGCGA 1467
      | |||| | || |||| | ||||| || ||||| || |||| | ||
Db      196 GCTGCGCGTCGATGCGGTGGCGTCAATGATTTATCGCGACTACAGCCGTAAAGAGGGGGA 137
Qy     1468 GTGGATTCCCAACCGCTACGGCGGCAGCGAAAATCTGGAAGCCATCGCCTTTTTCGCGCA 1527
      |||| | || || | |||| | || | |||| | || | || || |
Db      136 GTGGATCCCGAACGAATTTGGCGGGCGCGAGAATCTTGAAGCGATTGAATTCGAGCTCGG 77
Qy     1528 AACCAATGCCGTCTTAAAAAGCGA 1551
      ||| | || | || |
Db      76 TACCCGGGGATCCTCTAGAGTCGA 53

```

## RESULT 2

CG755637/c

LOCUS CG755637 1342 bp DNA linear GSS 24-OCT-2003  
 DEFINITION P051-1-G03.yc Ppa EcoRI BAC Library *Pristionchus pacificus* genomic,  
 genomic survey sequence.

ACCESSION CG755637

VERSION CG755637.1 GI:37982334

KEYWORDS GSS.

SOURCE *Pristionchus pacificus*ORGANISM *Pristionchus pacificus*

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
 Neodiplogasteridae; *Pristionchus*.

REFERENCE 1 (bases 1 to 1342)

AUTHORS Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,  
 Buntjer,J., van der Meulen,M. and Sommer,R.J.

TITLE An integrated physical and genetic map of the nematode *Pristionchus*  
*pacificus*